fells fells

057408 Q9DFV0 Q9PVD4 Q9IAR7 Q9XSZ8

Q9PW79 Q9DDD2 Q9PRG7

095ND3 09YP87 09WJB4

099MM1

088949 fells silve
096134 brachydanio
057408 meleadaris g
09dfv0 brachydanio
09pvd4 xenopus lae
09iar7 gallus gall
09xsz8 cercopithec
09pw79 gallus gall
09br97 xenopus lae
099mm mus musculu
09br97 xenopus lae
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057120 monkeypox v

Q8SQ34 Q8VD70

057122 057098 08UYA7 057284

Q9JKE0 O57120 O72735 Q911R5 O57123

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PRELIMINARY;
NCBI_TaxID=9541;
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01-MAY-2000 (
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429.5
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                                                   ; Search time 29.3505 Seconds
       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                 hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                      Listing first 45 summaries
                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1804
1 MLGIWTLLPLVLTSVARLSS.
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2: sp_bacteria:*
3: sp_fung1:*
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ALIGNMENTS

057119 057100 057102

Ogbain macaca tasc Ogbain macaca neme Ogbain errocebus Ogot36 macaca mula Ogot36 macaca assa Ogot88 macaca arct Ogbap octus trivi Ogbap octus trivi Ogot90 oryctolagus Ogyt90 oryctolagus Ogyt91 ovis aries Ogys60 oryctolagus Ogys60 oryctolagus Ogys60 oryctolagus Ogys60 fells silve Ogogh7 gallus gall macaca fasc macaca neme Description Q9tsn4 09R230 08SQ52 09DGH7 09DGH8 Q9TSN4 Q9BDN0 Q9BDN2 Q9GK36 Q9GL40 Q9GK28 Q9GK28 Q9GK28 097491 09XS60 8 Length Query 1552 1531 1531 1500 1492.5 1373.5 1052 1052.5 1052.5 481.5 478 463.5 Score

, , Murayama Y., Terao K., Incernity and M.;

Murayama Y., Terao K., Incernity and Murayama M.;

"Molecular clouding and characterization of cynomolgus monkey Fas.";

Hum. Immunol. 61.474.485(2000).

R EMBL; AB031420; BAA83551.1; -.

R HSSP; P25445; IDDF.

InterPool; IPR000488; Death.

InterPool; IPR00020; TRFLc6.

R Pfam; PF00020; TRFLc6.

R SMART; SM00035; DEATH; 1.

R SMART; SM00035; DEATH; 1.

R RART; SM00036; TNFR. 2.

R PROSITE; PS00552; TNFR NGFR_1: 1.

R PROSITE; PS00552; TNFR NGFR_1: 1. Gaps Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Usukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; 4 Length 331; Indels 331 AA; 37265 MW; OC617508081B05DF CRC64; (TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update) 86.0%; Score 1552; DB 6; 87.2%; Pred. No. 2.2e-121; ive 14; Mismatches 25; 331 PRT; SEQUENCE FROM N.A. MEDLINE-20237686; PubMed-10773350; Death receptor Fas (APO-1/CD95). Matches 292; Conservative Similarity Receptor. SEQUENCE Query Match

1 MLGIWTL.PLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60

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FAS antigen CD95
                                                                                                                                                            NCBI_TaxID=9531;
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SEQUENCE
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                        RIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL
                                                                LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
                                                                                                                                                                                          Macaca nemestrina (Pig-tailed macaque).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                Length 331;
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(TrEMBLrel. 21, Last annotation update)
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85.7%; Pred. No. 1.2e-119;
ive 17; Mismatches 27;
                                                                                                             ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                     Created)
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Matches 287; Conservative
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SEQUENCE FROM N.A.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Welss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 331;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, sequencing, and homology analysis of non Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).

EMBL; AF344843, AAK37602.1; EMBL; AF344844, AAK37602.1; Interpro: PR000188; Death.

Interpro: PR0001388; TWFR_c6.

Interpro: PR0001388; TWFR_c6.

Pfam; PF00020; TWFR_c6; 2.

SWART; SW00005; DEATH; 1.

SWART; SW00208; TWFR; 2.

PROSITE; PSS0017; DEATH_DOMAIN; 1.

PROSITE; PSS0017; DEATH_DOMAIN; 1.

PROSITE; PSS0017; DEATH_DOMAIN; 1.

PROSITE; PSS00105; TWFR_MGFR_1; 1.
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; Pred. No. 8.5e-119;
17; Mismatches 28;
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85.48;
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Matches 286; Conservative
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83.1%; Score 1500; DB 6;
84.2%; Pred. No. 4.8e-117;
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                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).
Sukaryota: Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                               nonhuman primate
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Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Welss W.R., Ansari A.A.;
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                                                                                                                                                                                                                                                                                                                        Welss w.r., Ansati A.A.;

"Cloning, sequencing, and homology analysis of non Fas/Fas-ligand and co-stimulatory molecules.";
Immunogenetics 53:315-338(2001).

EMBL, AR34483; AR437529.1;

HSSP, P25445; 1DDF.

InterPro; IPR000488; Daeth.

InterPro; IPR001368; TWFR_C6.

Pfam; PF00531; death, I.

Pfam; PF00531; death, I.

Pfam; PF005020; TWFR_C6; 2.

SMART; SM00005; DEATH; 1.

PROSITE; PS50017; DEATH; 1.

PROSITE; PS50055; TWFR_NGFR_1; 1.

PROSITE; PS50055; TWFR_NGFR_1; 1.

PROSITE; PS50055; TWFR_NGFR_1; 1.
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85.2%; Pred. No. 8.5e-118;
tive 16; Mismatches 28;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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01-JUN-2002 (TREMBLrel. 21, Last ann
FAS antigen CD95.
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SEQUENCE FROM N.A.
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                                                                                                                            Macaca assamensis (Assam's macaque) (Assam's monkey).

Bukaryota: Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                                                                                                                             Chi L., Shui B., Jiang H., He F.Q., Zhang Y.R., Cai Y.Y.; Chi L., Shui B., Jiang H., He F.Q., Zhang Y.R., Cai Y.Y.; "Cloning and sequencing of bear monkey Fas antigen cDNA."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AR235208; AAG49382.1; -. HSSP; P25445; IDDF.
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InterPro; IPR001368; INFR_c6.
InterPro; IPR001368; INFR_c6.
Pfam; PF00020; INFR_c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; INFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50052; INFR_NGFR_1; 1.
PROSITE; PS50052; INFR_NGFR_1; 1.
SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fas antigen APO-1/CD95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKD 297
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                                                                                                                                                                                                                                                                                                                                                               Gaps
                                         Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca arctoides (Stump-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                    Shuib., Child.... and Y.R.;

Shuib., Child... and Sequencing of Rhesus monkey Fas antigen CDNA.";

"Cloning and sequencing of Rhesus monkey Fas antigen CDNA.";

"Lowenthed (Aug-2000) to the EMBL/GenBank/DDBJ databases.

"RATO 7572. AAG16762.1; -...

"RASP: P25445; IDDF.

"RICEPPO: IPR000488; Death.

"RICEPPO: IPR000368; TUFR_c6.

"RAMAT; SM00005; DEATH; 1.

"SMART; SM00005; DEATH; 1.

"SMART; SM00005; DEATH; 1.

"SMART; SM00005; TUFR, 1.

"RAMAT; PS00652; TUFR_NGFR_1; UNKNOWN_1.

"R PROSITE; PS00652; TUFR_NGFR_2; 2.

"R PROSITE; PS00652; TUFR_NGFR_2; 2.

"R PROSITE; PS00650; TUFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                        L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                 Similarity 84.0
84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Chi L., Shui B., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9540;
                                  Fas antigen.
                                                                                                                                                                                                                                                                                                                            Matches 284;
                                                                                                                                                                                                                                                                                                        Query Match
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Q9GK28;
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121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                               181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonhuman primate
                                                                                                                                                                                                                                                                         DB 6; Length 310;
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MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                Query Match 79.8%; Score 1439.5; DB 6; Length Best Local Similarity 81.2%; Pred. No. 4.9e-112; Matches 272; Conservative 15; Mismatches 23; Indels
"Cloning of fas gene in stump-tailed monkey.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332357; AAG49394.1;
                                                                                                                                                                                                                                  C5C79BF1F804A419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning, sequencing, and homology analysis of Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
EMBL; AF344835; AAK37531.1; -...
InterPro; IPR000488; Death.
InterPro; IPR0001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aotus trivirgatus (Night monkey) (Douroucouli)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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                                                                                                                                                                         PROSITE; PS50017; DEATH_DOMAIN; 1
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 310 AA; 34806 MW; CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00531; death; 1.
Pfam; PF00507; death; 1.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00055; DAATH; 1.
SMART; SW00208; TNFR; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                   HSSP; P25445; IDDF:
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00021; death; 1.
Fram; PF00020; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
FAS antigen CD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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105 176 165

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220 AEEMKINEVKEFVRKNGVNEAKIDEIKNDNIQDTAEQKVQLLRNWHQLHGKKDAYNTLIK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 LCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIK 296
                                                                                                                                                                                                                                                                                                                                                     237 AGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIK 296
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ISONO T., Tanbe Y., Nagano Y., Seto A.;
ISONO T., Tanbe Y., Nagano Y., Seto A.;
Splicing and allelic variation in the rabbit Fas antigen gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021298; BAA78430.1;
HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotá; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
1-Ype Fas antigen.
07/yctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001368; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00131; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS0017; DEATH_DOMAIN; 1.
PROSITE; PS00502; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00505; TNFR_NGFR_1; UNKNOWN_1.
SEQUENCE 319 AA; 35961 MM; 06FA0033B1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 DLKKANLCTLAEKIQTIILKDITSDSENSNFRNE 330
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                                                                                                                                                                                                                                                                                                                                                                                                            RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGW-LCL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGV 239
                                                                                                                                                                                                                                                                                                                                                                              KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 MTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                           1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                         MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
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ISONO T., Tanbe Y., Nagano Y., Seto A.;
ISONO T., Tanbe Y., Nagano Y., Seto A.;
"Splicing and allelic variation in the rabbit Fas antigen gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021299; BAA78431.1; -.
EMBL; AB021296; BAA78428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                       13;
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                                                                                                                                           Ouery Match 76.4%; Score 1377.5; DB 6; Length 328; Best Local Similarity 78.7%; Pred. No. 7.6e-107; Matches 266; Conservative 21; Mismatches 38; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID-9986;
                                                         157 157 S -> T.
328 AA; 37332 MW; B3DEDIDAC97D6353 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВВ
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61.1%; Pred. No. 9e-80;
11ve 36; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00531; death; 1.
SWART; SW00203; TNFR_c6; 3.
SWART; SW00208; TNFR; 3.
PROSITE; PS50011; DEATH_DOMAIN; 1.
PROSITE; PS50050; TNFR_U6FR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_1; UNKNOWN_1.
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PS00652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 2.
157 157 S ->
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204;
                                                         VARIANT
PROSITE;
                                 PROSITE;
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Q9XS29;
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Matches
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01-DEC-2001 (
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Q9R230
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219 AEEMKINEVKEFVRKNGVNEAKIDEIKNDNIQDTAEOKVQLLRNWHQLHGKKDAYNTLIK 278
                                                                                                                                                                                                                                                                                                        Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.; "Cloning of sheep fas antigen.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ABOli671; BAA37093.1;
HSSP; P25445; IDDF.
InterPro; IPRO0488; Death.
InterPro; IPRO01888; TNFR_C6.
Pfam; PF000531; death; 1.
Pfam; PF000531; death; 1.
SMART; SM00005; DBATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLISNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.6%; Score 967; DB 6; L
Best Local Similarity 56.7%; Pred. No. 1.2e-72;
Matches 190; Conservative 47; Mismatches 90;
                                          297 DLKKANLCTLAEKIQTIILKDITSDSENSNFRNE 330
                                                                                                                    327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA.
                                                                                                                                             Created)
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00208; TNFR; 3
PROSITE: PS50017: DEATH_DOMAIN; 1.
PROSITE: PS00652; TNFR_MGFR_1; 1.
PROSITE: PS50050; TNFR_MGFR_2; 2.
SEQUENCE 327 AA; 36928 WW; SCR
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                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                TISSUE-LYMPHOCYTE,
                                                                                                                                                                                                                                                           NCBI_TaxID-9940;
                                                                                                                                                                                 Fas protein.
                                                                                                                097491
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Q9xs60;
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AC 097491 \( \)
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DE Fas p
GN Ovis
OC Bukar
OC Buvar
OC Bovid
RN ISDI
RN ISDI
RN ISDI
RN ISDI
DR EMBL;
DR EMBL;
DR INTER;
DR SMARTI
DR PFAM;
DR PFAM;
DR PROSI
SO SEQUE;
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Q9XS60
ID Q9XS60
AC Q9XS60
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61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 TIQNTKCRCKSNFFCNALKCEHCDPCTWCEHGIIEECTQTSNTKCKEKGSTTGSKHHFLW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SECOND T., Tanbe Y., Magano Y., Seto A.;
"Splicing and allelic variation in the rabbit Fas antigen gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
BRBL; AB021297; BAA78429.1;
HSSP: TANDATOR TO THE TAND
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Lareu R.R., Dharmarajan A.;
"Cloning and expression of Fas and Fas Ligand in the apoptotic rat
                                                                                                   Fas antigen spliced variant.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Score 614.5; DB 6; Length 53.8%; Pred. No. 2.3e-43; Live 23; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corpus luteum.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104034; AD20221.1;
HSPP; P25942; 1CDF.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS000652; TNFR, 10KNOWN_1.
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(TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 LCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPPO,02368; INFR_c6.
Pfam; PF00020; INFR_c6; 3.
SMART; SM00208; INFR; 3.
PROSITE; PS00052; INFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; INFR_NGFR_2; 2.
SEQUENCE 263 AA; 30374 MW; 6D76782ADE
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16644 MW;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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150 1
150 AA;
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                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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Search completed: May Sob time: 32.3505 secs
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                                                                                                                                                                                                                                                        ERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CMMCEHGILENCTPTSNTKCK-QGSSSKLLWLCALLLILPSAL------VCCCVLKK 110
                                                                                                                                                                                                                                                                                          58 ERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTRTQNTK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 CTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTC----RK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Fas ligand receptor soluble form (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                     7 LLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCHKPCPPG 66
                                                                                                                                                                       2 VLPLVLAG----PELINVRAQGTDSISEGLELKRSVRETDNNCSEGLYQVGPFCCQPCQPG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
Alternatively spliced transcripts of Fas mRNAs.in feline lymphoid
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas (Fragment).
Fells silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
                     DB 11; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.5%; Score 478; DB 6; Length 147; 55.1%; Pred. No. 2.7e-32; Live 24; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB072009; BAB86798.1; -. 1
NON_TER 1 1
NON_TER 1 147 147
SEQUENCE 147 AA; 16751 WW; 0E192AC4DCE1001F CRC64;
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147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                              ; Pred. No. 1.4e-32; 21; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 HRKENQGSHESPTLNPETVAINLSDVDLSKYITTIA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AA.
               26.7%; Score 481.5; 55.6%; Pred. No. 1.46
                                                                                                                                                                                                                                                                                                                                                                                                                CRCKPNFFCNSTVCEHCDPCTKCE-HGIIKECT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86; Conservative
                                                                             Conservative
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Matches 86; Conserv
                  Query Match
Best Local Similarity
Matches 85; Conserv
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SEQUENCE FROM N.A.
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Q9DGH7
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9, 2003, 17:06:47

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56 GQFCHKFCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 ------VKRKVNNYTTQGN---TAAADTGKVHSPETLRLIHIDVDLTHHVP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 EINCTRIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHG-IIKECTLTSNTKCKEEGSRSNL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 GWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYIT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.1%; Score 470; DB 13; Length 2 37.7%; Pred. No. 2.8e-31; Live 43; Mismatches 101; Indels
"Fas Expression and Regulation in Hen Granulosa Cells."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases: EMBL; AF206675; AAG02243.1; -... HSSP; O14765; 1D4V.
HSSP; O14765; 1D4V.
InterPro: IFR001488; Death.
InterPro: IFR001368; TNFR_C6.
Pfam; PF0005; 1; death; 1.
Pfam; PF0005; 1; MFR_C6; 2.
SMART; SM00050; DEATH; 1.
SMART; SM00050; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 AA; 32431 MW; A9761960CCD79E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 ICSLRDLKMRTAADKIERKLKAAVCSHQERRESYND 252
                                                                                                                                                                                                                                                                                                                                            PROSITE; PSEG017; DEATH_DOMAIN; 1.
PROSITE; PSG0652; TWFR_NGFR_1; UNKNOWN_1.
PROSITE; PSEG050; TWFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Human Fas antigen.
hFas from plasmid
Human Fas antigen.
Fas protein. Mamm.
Amino acid encodin
CD-95 (FAS/PO-1)
Human tumour necro

AAW50289 AAW49104

protein

Human Fas

Human Fas receptor Human Fas receptor Fas delta-TM. Hom Human Fas soluble Soluble Fas recept Rat Fas receptor. Human Fas. Homo s

AAB19341 AAB01335 AAB50517 AAB50657 AAB50893 AAR76238 AAR76238 AAR99682 AAB36228 AAB36228

Fas protein. Unid Human Fas receptor Expression vector Human colon cancer Fas antigen #1. S Human Fas antigen Human Fas antigen Antigenic acid selection (1944)

AAB53420

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856
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844
810.5
810.5
676.5
530
520
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494.5
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335
281
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220
 (without alignments)
801.926 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*
| SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*
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1804
1 MLWIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327
                                                                                                                       May 9, 2003, 16:57:39; Search time 54.3354 Seconds
                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

RESULT

Tumour necrosis fa Tumour necrosis fa Fas/Apo-1/CD95 Dea Fas-R protein frag

AAY97651 AAR99683 ABB81752 ABB81750 AAY97654

Flt-lextraFAStm/cy Flk-lextraFAStm/cy Apoptobody3sc fusi CD44Hextra/tmFAScy Human Fas soluble

AAR41688	TD AAR41688 standard: Protein: 327 AA	××	AC AAR41688;	. XX	DT 19-APR-1994 (first entry)	XX	DE Murine Fas.	XX	KW Murine; Fas; human; macrophage; cell strain; BAM3.	XX	OS Mus musculus.	PN JP05219959-A.		PD 31-AUG-1993.	XX	PF 14-FEB-1992; 92JP-0028090.		PR 14-FEB-1992; 92JP-0028090.	XX	PA (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.		-	DR N-PSDB; AAQ48008.		_	PT prepd. from e.g. BAM3 cell of mouse macrophage cell		PS Claim 1; Page 6-7; 8pp; Japanese.		CC This sequence represents the murine Fas protein. The cDNA encoding	
12: /SIDS2/qcqdata/qeneseq/qeneseqp-embl/Aa1991.DAT:*	/SIDS2/qcqdata/geneseq/geneseqp-embl/AA1	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1	16: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1995.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1	18: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1997.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1	`	22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*	23: /SIDS2/gcgdata/geneseq/genesegp-embl/AA2002.DAT:*		score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.		SUMMARIES	æ	lt Query	o. Score Match Length DB ID Description		100.0 327 14	16	100.0 327 17 AAR92530	100.0 327 21 AAB19344) 99.8 327 20 AAW86241	55.5 576 16 AAR78613	981 54.4 592 17 1	54.2 169 16 AAR78612	5 47.9 669 19 AAW64484	10 856 47.5 335 13 AAR28084 Human cell surface	

Result

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327 AA;
                                         related diseases
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                                                                                                                                                                                                                                                                                                                                              mFas sequence.
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                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                        Seguence
                                                                       Query Match
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                                                                                                                                                                                          PGKKKVEDCKMNGGIPTCAPCIEGKEYMDKNHYADKCRRCILCDEEHGLEVEINCILIQN 120
                                                                                                             Gaps
                                                                        1 MEWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
                                                                                Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                  Fas antigen; extracellular region; soluble membrane protein; iy production; diseases; treatment; prevention.
                                                                                                                                                                      this sequence hybridises with the human Fas gene and was isolated from the mouse macrophage cell strain BAM3. This sequence may be used for the production of large amounts of murine Fas.
                                                             ;
                                            100.0%; Score 1804; DB 14; Length 327; 100.0%; Pred. No. 4.1e-140; Pred. 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                     Murine Fas antigen extracellular region.
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/label= sig_peptide
22..327
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/label- mat_peptide
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                                           Query Match
Best Local Similarity 100.0
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
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N-PSDB; AAQ95302.
                             327 AA;
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antibody; autoimmune disease; SLE; lupus erythematosus.
      region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF
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                                                                                                                                                        100.0%; Score 1804; DB 16; 100.0%; Pred. No. 4.1e-140;
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/note= "signal
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                                                                                                                                                                        Best Local Similarity 100.
Matches 327; Conservative
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untisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein (Fap-1) expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents murine Fas (Apo-1). The specification describes artisense compounds which are targeted to the 5'-untranslate region, translational start site, translational termination region or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas ligand (Fast), or Fap-1 (Fas associated protein 1, protein tyrosine phosphatase). The antisense compounds are used to inhibit the expression of Fas, Fast or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as heptitis. They can also be used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1804; DB 21;
Pred. No. 4.1e-140;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fage 108-109; 116pp; English
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100.0%;
                                10-APR-2000; 2000WO-US09540.
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N-PSDB; AAC61859.
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Matches 327; Conserv
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                                                                                                                                                                                                                                                                                                                                 This sequence represents the mFas antigen used for the mFas.EXT, contained within the plasmid pME185. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monochoral antibody, as well as the standard soluble Fas antigen represented by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
Fas associated protein 1; protein tyrosine phosphatase; cancer;
autoimmune disease; inflammatory disease; lymphoma.
                                                                                                                                                        Immunoassay method for soluble Fas antigen in body fluids – for diagnosis of auto: immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                             Example 9; Page 80-82; 124pp; Japanese.
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   Yonehara
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                                                                                                                                                                                     diagnosis of auto: immune dis
systemic lupus erythematosus
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Matches 327; Conservative
Noquchi J,
                                                          WPI; 1996-087635/09.
N-PSDB; AAT16305.
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Hachiya T,
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Sequence Query Match

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Gaps

Indels 0; Length 327;

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Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLFILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of soluble membrane proteins – for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
                                                                               Expression vector; pME18S/mFas.EXT-AIC2A; murine Fas an' extracellular; region; AIC2A; soluble membrane protein; antibody production; diseases; treatment; prevention.
                                                 Expression vector pME18S/mFas.EXT-AIC2A protein prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1001; DB 16;
Pred. No. 8e-74;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Pages 36-38; 51pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.5%;
91.2%;
                                                                                                                                                                                                                                                                                               93JP-0267644.
              (first entry)
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                                                                                                                                                                                                                                                                                                                                    NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 91.2
nes 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PLVFI--YRKYRKR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PLKTLECYNDYTNR 194
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-202847/27.
N-PSDB; AAQ95306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 AA;
                                                                                                                                                       Mus musculus
                                                                                                                                                                                         JP07115988-A
                                                                                                                                                                                                                                                          26-OCT-1993;
                                                                                                                                                                                                                                                                                                 26-0CT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-1996
                                                                                                                                                                                                                           09-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                    This represents a Fas ligand (FasL) protein. This can be used in the method of the invention of killing of tumour cells which express the Fas receptor. The method comprises administering non-tumourigenic cells that express the FasL to kill the tumour cells. Rhabdomyosarcoma cells which express the Fas receptor can also be killed by administering myoblast cells that express the FasL. The methods can be used for the destruction of Fas receptor expressing tumour cells. They also provide a general immune provocation that stimulates the clearance of the tumour cells involving the infiltration of neutrophils into the area of administration of FasL-expressing cells and also the infiltration of receptor on cells. The methods can also be used for the detection of the Fas receptor on cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRTLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                            Killing tumour cells which express the Fas receptor - by administering non-tumourigenic cells that express the Fas ligand to kill the tumour cells, e.g. rhabdomyosarcoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1800; DB 20;
Pred. No. 8.8e-140;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                          Killing tumour cells which express the
                                                                                                                                                                                                                                                                                                                                                                              Examples; Pages 23-25; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFQDMVQKDLGKSTPDTGNENEGQCLE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78613 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%;
ilarity 99.7%;
Conservative 1
                                                                                                                98WO-US07235
                                                                                                                                                 97US-0041880
                                                                                                                                                                                  (STRD ) UNIV STANFORD
                                                                                                                                                                                                                     Hofmann A;
                                                                                                                                                                                                                                                    WPI; 1999-009332/01.
N-PSDB; AAV71961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 AA;
                                        WO9846242-A1
                                                                                                              10-APR-1998;
                                                                                                                                                 11-APR-1997;
                                                                             22-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 326;
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Sequence

61

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61 121 241

241 301 301

181 181

AAR78613;

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AAR78613 ID AAR7 XX AC AAR7 RESULT

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Gaps

5;

Length 576; Indels

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Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation; agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; infection; graft rejection; antagonist; inhibitor; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                             Preparation of soluble membrane proteins – for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ95305 is the plasmid fragment pME18S which encodes AAR78612. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
antibody production; diseases; treatment; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 977; DB 16;
100.0%; Pred. No. 1.7e-72;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Pages 34-35; 51pp; Japanese.
                                                                             /label= sig_peptide 22..169
                                                            Location/Qualifiers
                                                                                                         22..169
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64484 standard; Protein; 669 AA
                                                                                                                                                                                                                                                  93JP-0267644.
                                                                                                                                                                                                                    93JP-0267644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                   (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                               WPI; 1995-202847/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TNFR1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 AA;
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ95305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related diseases
                                                                                                                                                         JP07115988-A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9832856-A1
                                                                                                                                                                                                                      26-OCT-1993;
                                                                                                                                                                                                                                                   26-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-1998.
                                                                                                                                                                                      09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 169;
                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW64484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                         Peptide
                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              These soluble Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The kit is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen is included in the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as one of these standard soluble Fas antigens. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR92526 and AAR92527 represent soluble Fas antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pME18S; soluble membrane protein; fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 981; DB 17;
Pred. No. 3.7e-72;
5; Mismatches 14;
                                                            /note- "mature Fas antigen #2"
                                                                                                                                                                                                                                     (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid fragment pME18S expression prod
                            /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 87-91; 124pp; Japanese.
   Location/Qualifiers
                                                                                                                                                                                                                                                                                    Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR78612 standard; Protein; 169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.4%;
89.2%;
                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosus
                                                                                                                                                                                        95JP-0025637
                                                                                                                                                         95WO-JP00349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.2
Matches 173; Conservative
                                              . 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PLVFI--YRKYRKR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 PLKTLECYNDYTNR 194
                                                                                                                                                                                                                                                                                    Noguchi J,
                                                                                                                                                                                                                                                                                                                WPI; 1996-087635/09.
N-PSDB; AAT16301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1996
                                                                                                                                                                                                       06-JUL-1994;
                                                                                                                                                         03-MAR-1995;
                                                                                             WO9601277-A1
                                                                                                                                                                                        14-FEB-1995;
                                                                                                                           18-JAN-1996
                                                                                                                                                                                                                                                                                    Hachiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78612;
                Peptide
                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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Gaps

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Fas antigen; apoptosis; pF58; NGFR/TNFR family.
                                                                                                                       /label= N-glycosylation_site
/note= "putative"
                                                                                                                                                         /label= N-glycosylation_site
                                                                                                  /label= Fas_antigen
                                                          Location/Qualifiers
                                                                                                                                                                  'note= "putative"
                                                                    1..16
/label= signal
                                                                                                              118..120
                                                                                                                                                                             .190
                                                                                                                                              136..138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 49.49
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-358914/44.
N-PSDB; AAQ29959.
                                                                                                                                                                                                                                                                                                                                                                       Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 AA;
                                                                                                            Modified-site
                                                                                                                                           Modified-site
                                   Homo sapiens
                                                                                                                                                                                                                                                                                                       24-APR-1992;
                                                                                                                                                                                                                                                                                                                            26-APR-1991;
                                                                                                                                                                                                                                                                                    28-OCT-1992
                                                                                                                                                                                                                                                               EP510691-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                  Peptide
                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                      Itoh N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                             Domain
                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                 Domain
                                                       Key
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                                                                                                                                                                                            This sequence represents a human tumour necrosis factor receptor-1 which is used in a method resulting in the isolation of a human death domain containing receptor 4, DR4 agonists are used to increase apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of graft vs. host disease, acute or chronic graft rejection, inflammation, DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune schaemed in the neurodegenerative disease, myelodysplastic syndrome, neurodegenerative disease, myelodysplastic syndrome, anorexia, also a wide range of inflammatory conditions. DR4 of fragments of the protein are used diagnostically, e.g. to detect mutant forms of DR4 (possibly associated with disease), for isolating the DR4 gene or related sequences and for chromosomal mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                          QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 IQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                 id encoding human death domain-containing receptor 4 - therapeutic modulation of apoptosis, in e.g. cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLLIPLVFIYRKYRKRKCWKRRQDDP --- ESRTSSRETIPMNASNLSLSKYIPRIAEDMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                      47.9%; Score 863.5; DB 19; Length 669;
49.2%; Pred. No. 1.9e-62;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                           54; Mismatches 108;
                                                                                           Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 NLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                          Pan JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR28084 standard; Protein; 335 AA.
                                                                                                                                                                          Disclosure; Fig 2; 92pp; English.
                                                     (HUMA-) HUMAN GENOME SCI INC
   98WO-US01464
                       970s-0037829.
970s-0035722.
                                                                                         Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                (UNMI ) UNIV MICHIGAN.
                                                                                                                                 Nucleic acid encoding
                                                                                       Gentz RL,
                                                                                                            WPI; 1998-427952/36.
                                                                                                                                                       autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                669 AA;
                      05-FEB-1997;
28-JAN-1997;
   27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 164;
                                                                                                                                              useful for
                                                                                      Dixit VM,
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR28084;
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LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Fas antigen is implicated in apoptosis. A cDNA clone encoding the antigen was isolated (PF58) and the amino acid sequence of Fas was deduced from it. The mature protein has a calculated mol.wt. of 36,000 and is a member of the NGFR/TMFR family of cell-surface membrane proteins. The inventors claim a protein comprising at least the extracellular domain of Fas antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 856; DB 13;
49.4%; Pred. No. 3.4e-62;
iive 54; Mismatches 107;
                   17..173
/label= extracellular
/note= "cysteine-rich"
'label≕ transmembrane
                                                                                                             /label- cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                       Yonehara S;
                                                                                                                                                                                                                                                                                                                                    (OSAB-) OSAKA BIOSCIENCE INST
                                                                                                                                                                                                                                                                                            91JP-0125234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 1 and 2; 27pp;
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AAR99681 standard; Protein; 335
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                               Human Fas artigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT34526
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                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                AAR99681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                   Domain
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          181
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           177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLWIWAVLPLVLAG ----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR78606 (human Fas protein) is encoded by the plasmid pF58 which contains hFas cDNA. The plasmid was used in the construction of an expression vector for the prode. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT
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                                                                                                                                                                                                                  soluble membrane protein;
                                                                                                                                                                                                                              treatment; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 47.5%; Score 856; DB 16; Best Local Similarity 49.4%; Pred. No. 3.4e-62; Matches 165; Conservative 54; Mismatches 107;
                                          AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                          Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                     1..16
/label= sig_peptide
17..335
/label= mat_peptide
                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                        AAR78606 standard; Protein; 335
                                                                                                                                                                                                                 Plasmid pF58; human Fas cDNA; s
antibody production; diseases;
                                                                                                                                                                                                                                                                                                                                                                                         93JP-0267644
                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0267644
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                                                                                                                                                                     (first
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                                                                                                                                                                                            Human Fas protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 AA;
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                                                                                                                                                                     19-FEB-1996
                                                                                                                                                                                                                                                    Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                  09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1;
                                                                                                                                              AAR78606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                           Peptide
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                                          293
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TIQEAKRFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
                            A cDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas antigen (AAR9681). It was isolated from cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy (ALLD) patients. 4 Soluble variants (AAR99682-85) were identified of the Fas antigen. These arose by alternative splicing of Fas gene transscripts. The Fas variants were present at higher levels in SLE and ALLD patients than the non-soluble Fas antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 335;
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Pred. No. 3.4e-62;
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191..335
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                                                                                                                   AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                                                                                       ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
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/label= Cytoplasmic_tail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou T;
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/label- Sig_peptide
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/label- Mat_protein
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      3;
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                                                                                                                                                                                                                                                                                                                                  antibody; autoimmune disease; SLE; lupus erythematosus.
                                                   57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                      LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                Gaps
                                       9
                1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC
                           VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM
                                                                                                                                   TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoassay method for soluble Fas antigen in body fluids – for diagnosis of auto:immune diseases such as rheumatoid arthritis and systemic lupus erythematosus
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54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                          /note= "hFas signal peptide"
                                                                                                                                                                                            293 AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                                                                                                                                        ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
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                                                                                                                                                                                                                                                                                                                               Fas; antigen; immunoassay; monoclonal rheumatoid arthritis; serum; systemic
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yonehara
                                                                                                                                                                                                                                                                                                              hFas from plasmid pCEV4/hFas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95JP-0025637.
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                                                                                                                                                                                                                                                                                             (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noguchi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-087635/09.
N-PSDB; AAT16303.
                                                                                                                                                                                                                                                                                            06-SEP-1996
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06-JUL-1994;
165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hachiya T,
                                                                                                                                                                                                                                                                                                                                                         Synthetic
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Matches
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the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as the standard soluble Fas antigen represented by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                            117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                             QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                                                                                                                                                                                                                                                                                                     177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis regulation; gene therapy;
lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                    1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC
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8
                                                                                                                                                                                     Length 335;
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                                                                                                                                                                              47.5%; Score 856; DB 17;
49.4%; Pred. No. 3.4e-62;
clve 54; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANLCTLAEKIQTILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "claimed fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label sig_peptide 17.335 /label mat_peptide 17.173 /note= "claimed fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Socation/Qualifiers
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treatment; diabetes; arthritis;
apoptosis modulation.
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                            Local Similarity
les 165; Conserv
                                                                                                                                                    335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Fas antigen.
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                                                                                                                                                   Sequence
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW50289;
                                                                                                                                                                                            Best Local
Matches
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Peptide
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                                                                                                                                                                                                                                                                                             57
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The present sequence represents a Fas protein sequence used in the method of the invention. The method is concerned with reducing depictation of activated Fas-expressing CD8+ T-Iymphocyte Killer (TK) cells in an immune cell population which also comprises of Fas-ligand cells in an immune cell population which also comprises of Fas-ligand immune cell population which well as agent (e.g. a soluble Fas-Fc fusion protein) which would interfere with the interaction between Fas and FasL. Therefore, the method is useful for interaction between Fas and FasL. Therefore, the method is useful for identifying suitable agents which can reduce depletion of activated CG Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions. Associally surface receptor Fas and its ligand FasL. By interfering with this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of FasL on activated CD4+ cells. Such FasL-expressing activated CD4+ cells are especially the result of CD4+ cell infection with an immunodeficiency virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). The claimed prevention of apoptosis and the CD4+ cells infected with the infectious agent, enabling treatment (prophylactic and/or therapeutic) of immunodeficiency is a firement of the company than allow the company company company companies of the company companies of the compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTONTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKOSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLGIWILLPLVLISVARLSSKSVNAQVIDINSKGLELRKIVTIVETQNLEGLHHDGQFCH 60
                                                                                                                                                            fused to a Fc polypeptide to form a Fas-Fc fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLWIWAYLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing CDE+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 856; DB 19;
49.4%; Pred. No. 3.4e-62;
tive 54; Mismatches 107;
                                                                                                                          /note= "Fas protein"
17..172
/note= "The portion of a Fas
                                                                      "Signal peptide"
                                                                                           ..335
..te= "Fas protein"
                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                  98WO-GB00485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV; simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL; prophylactic; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
                                                                                                                                                                                                                                                                                                                                                                          antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the lst cysteine residue (preferably at least 29 residues are deleted).

The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8,
                                                                                                                                                                                                                                                                                                                                                     present sequence was used in the development of novel Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%; Score 856; DB 18; Length 3.49.4%; Pred. No. 3.4e-62; Live 54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                                                                                                                                                   Claim 2; Fig 1-2; 102pp; Japanese.
(MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST
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Matches 165; Conservative
                                                                        Nagata S, Nakamura N;
                                                                                                                       WPI; 1997-558981/51.
N-PSDB; AAV07002.
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Sequence Query Match

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Length 335;

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RESULT 1:

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177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
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Search completed: May 9, 2003, 17:05:11 Job time : 61.3354 secs

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May 9, 2003, 17:03:26; Search time 12.8429 Seconds (without alignments) 749.153 Million cell updates/sec
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1804
1 MLWIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                      262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

RESULT 2 US-09-013-895A-3

Sequence 23, Sequence 22, Sequence 10, Sequence 11, Sequence 11, Sequence 13, Sequence 3, Sequence 3, Sequence 2,	Fas Mediated	Length 327; Indels 0; G EGLYQGGPFCCQPCQ	SLYGGPFCCQPCQ HGLEVETNCTLTQN 	RNRLWLLTILVLLI 180 RNRLWLLTILVLLI 180	RIAEDMTIQEAKKF 240	IKGLKKAECRRTLD 300 IKGLKKAECRRTLD 300	
4 US-09-180-100-23 4 US-09-180-100-9 4 US-09-180-100-10 4 US-09-180-100-10 4 US-09-180-100-11 4 US-08-828-683A-15 2 US-08-219-2378-3 2 US-08-219-2378-3 4 US-08-477-347-14 4 US-08-477-347-14 4 US-08-477-347-14 4 US-08-477-385-26 1 US-08-444-005-32 4 US-09-444-005-32 4 US-09-656-918-2 1 US-09-444-005-26 4 US-09-086-483A-6 4 US-09-086-483A-6	ALLUNMENTS 9290640 Compound Modulation of US/09/290,640 .	0%; Score 1804; DB 4; 0%; Pred. No. 6.7e-158; 0; Mismatches 0; ITQGTNSISESLKLRRRVHETDKNCS	MLMIWAVLPIVLAGSQLRVHTQGTNSISESLKIRRRVHETDKNCSEGLYGGGFFCCQP PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLT 	TKCKCKEDEYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKOSPRNRLWLLTILVLLI 	PLVFIYFKYRKRKCWRRRQDDPESRTSSRETIPWNASNLSLSKYIPRIAEDWIIQEAKKF 	ARENNIKEGKIDEIMHDSIODTAEOKVOLLLCWYQSHGKSDAYODLIKGLKKAECRRTLD 	ENEGOCLE 327 . ENEGOCLE 327
2 27.4 159 27.4 159 26.1 143 376 26.1 143 376 26.1 143 376 25.5 1119 25.5 119 25.5 1119 25.5 119 25.5 1119 25.5 1119 25.5 1119 25.5 1119	4Eplication (2006) Application (h Similarity 100 27; Conservative WIWAVLPLVIAGSOLRVI	IWAYLPLYLAGSQLRYI KKVEDCKMNGGTPTCA 	KCKFDFYCDSPGCEHC' 	FIYEKYRKRKCWKRRQI 	NNIKEGKIDEIMHDSI(KFQDMVÇKDLGKSTPDTGNENBGQCLE
28 494.5 30 494.5 30 470 31 470 32 462 33 462 34 460 36 460 37 460 38 460 39 230 40 218 41 215 42 215 43 215 44 210.5	RESULT 1 US-09-290-640- Sequence 66, Patent No. 6 GENERAL NO. 6 GENERAL TITLE APPLICANT: CURRENT FILE CURRENT FILE CURRENT FILE CURRENT PIL CURRENT FILE CURREN	Query Ma Best Loc Matches	Db 1 MEW Qy 61 PGKI Db 61 PGKI	121	Qy 181 PLVI Db 181 PLVI	Qy 241 AREI Db 241 AREI	Qy 301 KFQI Db 301 KFQI

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US-09-448-868-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                          TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: TITLE OF INVENTION: Receptor 4), Member of the INF-Receptor NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/013,895A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.9%; Score 863.5; DB 4;
49.2%; Pred. No. 4.2e-71;
tive 54; Mismatches 108;
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                                                                                                                                                                                SEE: HUMAN GENOME SCIENCES, INC: 9410 KEY WEST AVENUE ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                       1488.1300002
3, Application US/09013895A
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATTON NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                     Ni, Jian
Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
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(202)371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.28
Matches 164; Conservative
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                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GEN
          Patent No. 6342363
GENERAL INFORMATION:
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CLASSIFICATION:
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20850
                                                                              APPLICANT:
APPLICANT:
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                                     APPLICANT
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Death Domain Containing Receptor 4 (DR4: Death Receptor 4), Member of the TNF-Receptor Superfamily and Binding to Trail (AP02-L)
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47.9%; Score 863.5; DB 4; Length (Best Local Similarity 49.2%; Pred. No. 4.2e-71;
Matches 164; Conservative 54; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE: HEREWITH

CLASSIFICATION:
                                                                                                                                                                                                  STREET: 9410 KEY WEST AVENUE
STREET: 9410 KEY WEST AVENUE
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1488.1300004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1488.13C
TELECOMMUNICATION INFORMATION:
Sequence 3, Application US/09448868
Patent No. 6461823
                                                     APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
TELEPRAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STRANDEDNESS: si
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                                  GENERAL INFORMATION:
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salk, Werner
APPLICANT: Oehm Alexander
APPLICANT: Daniel, Personer T. T. TITLE OF INVENTION: Monoclonal Antibodies to the APO-1 Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5%; Score 856; DB 2; 49.4%; Pred. No. 8.3e-71;
| :| |:| |: || 301 ANLCTLABEKIQTILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTR89-35A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,644
FILING DATE: 16-JUN-1994
APPLICATION NUMBER: US 07/691,016
FILING DATE: 17-JUN-1991
CLASSIFICATION: 424
                                                                                                                                                                     APPLICANT: Krammer, Peter H.
APPLICANT: Debatin, Klaus-Michael
APPLICANT: Trauth, Bernhard C.
                                                                                         US-08-409-338-1; Sequence 1, Application US/08409338; Patent No. 5891434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                               Dhein, Jens
Klas, Christiane
M ller, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                             Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                 Behrmann, Iris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Militia I
CITY: Lexington, MA
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02173
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Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: TOOH, Naoto
APPLICANT: IYOKHARA, Shin
TILE OF INVENTION: ADA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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; Pred. No. 8.3e-71;
54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
PRIOR ADDITATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                           636 NLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 668
               294 ECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY ACENT INFORMATION:
NAME: James W. Hellwege
RECISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
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US-08-219-237B-2
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                  QPCQPGKKKVEDCKMNGGIPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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49.4%; Pred. No. 8.3e-71;
tive 54; Mismatches 107; Indels
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Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEL, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: RUBEN, STEINER
APPLICANT: RUBEN, STEINER
APPLICANT: TUMOR NECROSIS FACTOR RECEPTOR 5
                                                                                                                  293 AECRILDKFQDMVQKDLGKSTPDIGNENEGQCL 326
                                                                                                                                      ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
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301 ANLCTLAEKIQTILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                                                                       Sequence 2, Application US/09290640 Patent No. 6204055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4%
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 335
                                                                                                                                                                                                        US-09-290-640-2
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Pred. No. 8.3e-71; 11ve 54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: TONEHARA, Shin
ITILE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
ITILE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 AECRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ANLCTLAEKIQTILLKDITSDSENSNFRNEIQSL 334
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.5%; Score 856;
                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08468560C Patent No. 6270998 GENERAL INFORMATION:
                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.48
Matches 165; Conservative
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                             435
                                                                                                                                                      COMPUTER: IBM PCOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                             20850
                                                                                                                                                                                                 SOFTWARE:
                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-006-353A-7
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US-08-468-560C-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-565-918-3
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Best Local Similarity
Matches 165; Conserv
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SEQ ID NO 20
LENGTH: 335
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Patent No. 6306395

GENERAL INFORMATION:

APPLICANT: NAKAWURA, No. 630639510

APPLICANT: NAKAWURA, NO. 630639510

TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE

FILE REFERENCE: 1110-207P

CURRENT APPLICATION NUMBER: US/09/180,100

CURRENT FILING DATE: 1998-11-02

EARLIER RAPPLICATION NUMBER: PCT/JP97/01502

EARLIER RAPLICATION NUMBER: PCT/JP97/01502

EARLIER FILING DATE: 1997-05-01

NUMBER OF SEQ ID NOS: 25
                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                     20-4393P
                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 0
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION UNDBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4
TELECOMMUNICATION INFORMATION:
TELEFHONE: 703-205-8000
TELEFAX: 703-205-805
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 335 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-2
STREET: P.O. BOX 747
                FALLS CHURCH
                                                                      22040-0747
                                                     USA
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                                                     COUNTRY:
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                                                                                                                                                                          117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                             121 RIQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                       177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
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                                                                                                          1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
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     Length 335;
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Query Match 47.5%; Score 856; DB 4; Length 33 Best Local Similarity 49.4%; Pred. No. 8.3e-71; Matches 165; Conservative 54; Mismatches 107; Indels
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APPLICANT: No. Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, Jannes G.
APPLICANT: Goltz, Reiner L.
APPLICANT: Goltz, Reiner L.
APPLICANT: Goltz, Reiner L.
APPLICANT: Goltz, Reiner L.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT FILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 3
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Llarity 49.4%; Pred. No. 8.3e-71;
Conservative 54; Mismatches 107
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Patent No. 643347
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Sequence 2, Application PC/TUS9517083 GENERAL INFORMATION:
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Matches 165; Conserv
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                                                                                                              CLASSIFICATION:
                                                                                                 FILING DATE:
                                                                                                                                                                                                             TOPOLOGY:
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
               VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                                                                                                                                              233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
                                                                                                                                                             QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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' Pred. No. 8.3e-71;
54; Mismatches 107; Indels
                                                                                                                                                                                              293 AECRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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APPLICANT: N1, Jian
APPLICANT: N1, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Rec
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
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Patent No. 6455040
GENERAL INFORMATION:
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Best Local Similarity 49.48
Matches 165; Conservative
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US-09-573-986-7
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SEQ ID NO 7
LENGTH: 335
                                                                                                                                                                                                                                                           RESULT 11
US-09-573-986-7
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PCT-US95-17083-2

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117 LTONTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT
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49.4%; Pred. No. 8.3e-71;
Live 54; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
APPLICANT: CONTAINING Receptors
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                  SECRETED HUMAN FAS ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                                      USSN 08/371,263
                                                                                                  UMBER: PCI/US95/17083
CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
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                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
APPLICANT:
TITLE OF INVENTION: SECRE:
WUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT.
                                                                                                                                                                                                                                                                           : 335 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.7%; Score 825; DB 4; Length 33
49.9%; Pred. No. 5.7e-68;
Live 53; Mismatches 101; Indels
                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,936
FILING DATE: MAY-30-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08444231
Patent No. 5652210
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (301) 309-8504"
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.7%
Best Local Similarity 49.9%
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                       FILING DATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-086-483A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-444-231-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIQNIKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCIAISNINCRKQSPRNRLWLLIIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 OPCOPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NI, et al.
TILLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TRIO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1.1e-69; 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                     1488.0310003/EKS/KRM
                                                                         APPLICATION NUMBER: No. 6153402 Yet Assigned FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA: 4PPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.8%; Score 844;
49.1%; Pred. No. 1
US/08/815,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09086483A
Patent No. 6214580
                                                                                                                                                                                                                                                       NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 335 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                             202-371-2540
                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
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US-09-086-483A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-815-469-6
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QPCQPCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 IQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHCKSDAYQDLIKGLKKA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 ESQVKCFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 314;
                                                                                                                           COMPUTER: TBM FC Compatible
OPERATING SYSTEM: C-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.9%; Score 810.5; DB 1;
46.8%; Pred. No. 1.2e-66;
tive 50; Mismatches 100;
                                                                                                                                                                                                                                                  PRIOR ADDITION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 ECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                      (415) 813-5600
(415) 494-0792
                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 314 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-444-231-19
                                  Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 156; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                        ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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9, 2003, 17:08:25 Search completed: May Gob time: 13.8429 secs

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May 9, 2003, 17:05:23 ; Search time 16.3006 Seconds (without alignments) 1846.092 Million cell updates/sec
                                                                                                                                                                                                                                                                      1 MLWIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                      349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                           US-09-446-634A-23
1804
                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                   Perfect score:
                                                                                          OM protein
                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                     Run on:
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_DUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/ptodata/2/pubpaa/US07_NEW_PUB.pep:*/ptodata/2/pubpaa/US07_NEW_PUB.pep:*/ptodata/2/pubpaa/US07_PUBCOMB.pep:*/ptodata/2/pubpaa/US08_PUBCOMB.pep:*/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/ptodata/2/pubpaa/US09_NEW_PUB.pep:*/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/cgn2_6/ /cgn2_6/ /cgn2_6/

/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

Published_Applications_AA:*

Database

Result Ouery No. Score Match Length DB ID 1 1804 100.0 327 10 US-09-802-669-66 Sequence 66, Appl 2 166 64.6 204 10 US-09-948-018-18 Sequence 3, Appl 3 659 9 US-10-226-286-3 Sequence 3, Appl 5 655 47.9 669 9 US-10-226-318-3 Sequence 3, Appl 6 69 9 US-10-226-318-3 Sequence 3, Appl 6 69 9 US-10-226-318-3 Sequence 3, Appl 7 856 47.5 335 10 US-09-802-669-2 Sequence 2, Appl 1 0 US-09-802-69-2 Sequence 2, Appl 1 0 US-09-802-69-3 Sequence 2, Appl 1 0 US-09-802-69-2 Sequence 3, Appl 1 0 US-09-802-69-2 Sequence 6, Appl 1 0 US-09-914-91-2 Sequence 6, Appl 1 0 US-09-914-91-2 Sequence 3, Appl 1 0 US-09-914-91-2 Sequence 3, Appl 1 0 US-09-914-91-2 Sequence 3, Appl 1 0 US-09-91-313-96-6 Sequence 3, Appl 1 0 US-09-91-2-29-960 Sequence 3, Appl 1 0 US-09-91-2-299-960 Sequence 960, Appl 1 0 US-09-925-299-960 Sequence 960, Appl 1 0 US-09-925-299-960 Sequence 15, Appl 1 US-09-925-299-960 Sequen

Seguence 21, Appl	Sequence 23, Appl	Sequence 22, Appl	Sequence 9, Appl1	Sequence 10, Appl	Sequence 11, Appl	Sequence 15, Appl	Sequence 5, Appli	m	Sequence 14, Appl	4	4	à	Sequence 2, Appl1		4	Sequence 2, Appl1	1,	7	Sequence 13, Appl	Sequence 31, Appl	Sequence 2, Appl1	Sequence 2, Appl1	17,	Sequence 17, Appl	Sequence 30, Appl	
10 US-09-949-713-21			10 US-09-949-713-9	10 US-09-949-713-10	10 US-09-949-713-11	9 US-10-112-793-15	10 US-09-800-909-5	10 US-09-884-987-3		9 US-09-992-964-14	10 US-09-887-879-14	9 US-10-226-296-2	_	12 US-10-039-785-1	0	10 US-09-855-266A-2	10 US-09-855-266A-1	10 US-09-924-231-2	10 US-09-934-289A-13	10 US-09-935-727-31		12 US-10-066-209-2	9 US-09-992-964-17	10 US-09-887-879-17	10 US-09-782-980-30	
144	159	376	128	143	360	119	119	119	119	418	418	468	468	468	11	148	176	283	283	283	283	283	11	11	272	
27.4	27.4	27.4	26.1	26.1	26.1	25.6	25.5	25.5	25.5	11.9	11.9	11.9	11.9	11.9	11.6	11.4	11.4	11.4	11.4	11.4	11.4	11.3	11.2	11.2	11.2	
494.5	9	494.5	470	470	470	462	460	460	460	215	215	215	215	215	209	205	205	205	205	205	202	204	202	202	202	
20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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APPLICANT: Dear, Nicholas M.
APPLICANT: Dear, Nicholas M.
APPLICANT: Warcusson, Eric G.
APPLICANT: Warcusson, Eric G.
APPLICANT: Warcusson, Eric G.
APPLICANT: Warcusson, Eric G.
APPLICANT: Stang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: 158PH-345
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SET DATE OF SEQ ID NOS: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1804; DB 10; Length 327; 100.0%; Pred. No. 8.6e-125; ive 0; Mismatches 0; Indels 0;
                 Sequence 66, Application US/09802669
Patent No. US20020004490A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Mus musculus
US-09-802-669-66
                                                                  GENERAL INFORMATION
-09-802-669-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 327
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US-10-226-318-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death Receptor 4), Member of the TNF-Receptor Superfamily and Binding to Trail (AP02-L)
                                                 241 ARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRTLD 300
                                                                     181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEBHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGKKKVEDCKMNGGIPICAPCIEGKEYMDKNHYADKCRRCILCDEEHGLEVEINCTLIQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
Sequence 18, Application US/09948018
Patent No. US20020150977A1
GENERAL INFORMATION:
APPLICANT: THE AL
TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
FILE REPERBME: 01017/37677
CURRENT APPLICATION NUMBER: US/09/948,018
CURRENT FILING DATE: 2001-09-05
PRIOR PAPLICATION NUMBER: US 60/230,191
PRIOR FILING DATE: 2000-09-05
NUMBER OF SED ID NOS: 45
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.6%; Score 1166; DB 10; 100.0%; Pred. No. 2.8e-78;
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ADDRESSE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                         301 KFQDMVQKDLGKSTPDTGNENEGQCLE 327
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Publication No. US20030036168A1
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Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.
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Matches 204; Conservative
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APPLICANT: N1, Jian
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US-09-948-018-18
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US-09-948-018-18
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TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death Receptor 4), Member of the TNF-Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VLLIPLVFIYRKYRKKKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDMT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

47.9%; Score 863.5; DB 9;
Best Local Similarity 49.2%; Pred. No. 1.5e-55;
Matches 164; Conservative 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                 APPLICATION NUMBER: US/09/448,868
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
ATTORNEY/AGBWT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,296
FILING DATE: 23 Aug-2002
CLASSIFICATION: <a href="mailto:current-number">current-number</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 ECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-10-226-296-3
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Dixit, Vishva M.
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Rosen, Craig A.
Pan, James G.
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                                                                                                                                                                              PRIOR APPLICATION DATA:
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Sequence 2.2 Application US/09802669
Factor No. US2020004490A1
GENERAL INFORMATION:
FAPPLICANT: Dean, Nicholas M.
APPLICANT: Myatt, Jacqueline
APPLICANT: SIPH-545
CURRENT: EINFRITON ANDER: US/09/802,669
FRIOR FILING DATE: 2001-03-09
FRIOR PLING DATE: 2000-09-18
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: 1999-04-12
FRIOR FILING DATE: IN OS: 180
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                                    APPLICANT: Gentz, Reiner
APPLICANT: Rulen, Steven
APPLICANT: Nulen, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor
FILE REFERENCE: 1488-1280006
CURRENT APPLICATION NUMBER: US/09/826,212
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 856; DB 10;
Pred. No. 2.5e-55;
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SEQ ID NO 2
LENGTH: 335
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-7
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Best Local Similarity
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49.2%; Pred. No. 1.5e-55;
Live 54; Mismatches 108; Indels 7
                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/10/226,318
FILING DATE: 23-Aug-2002
CLASSIFICATION: <UNknown>
PRIOR APPLICATION: <UNknown>
APPLICATION NUMBER: US/09/448,868
FILING DATE: <UNknown>
APPLICATION NUMBER: US/09/448,868
FILING DATE: 27-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, RRIC K.
Superfamily and Binding to
                                                        ADDRESSEE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
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Patent No. US20010021516A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                     SEQUENCES: 12
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Best Local Similarity 49.2%
Matches 164; Conservative
                                                                                                   CITY: ROCKVILLE STATE: MD
                                                                                                                                            COUNTRY: US
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-826-212-7
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                     293 AECRRILDKFODMVQKDLGKSTPDTGNENEGQCL
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                                                                                              117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                      VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
                                                                                                                                                                                                             TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
                                                                                                                                                                                                                                                              1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
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TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NOWER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR APPLICATION NUMBER: DS/09/180,100
PRIOR APPLICATION NUMBER: DS/09/180,100
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
 Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.5%; Score 856; DB 10;
49.4%; Pred. No. 2.5e-55;
Live 54; Mismatches 107;
                                                                                                                                                                                                                                                                                                    293 AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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Patent No. US20020044944A1
GENERAL INFORMATION:
 54;
Conservative
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SOFTWARE: Patentin Ver. 2.9
SEQ ID NO 20
LENGTH: 335
TYPE: PRT
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JS-09-949-713-20
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Best Local Similarity
Matches 165; Conserv
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Matches 165;
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                           APPLICANT: Gentz, Reiner L.
APPLICANT: Yu, Guo-liang
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor
FILE REFERENCE: 1488.1310006
CURRENT APPLICATION UNDRER: US/09/874,138
CURRENT FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
47.5%; Score 856; DB 10;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107;
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PRIOR APPLICATION NUMBER: 60/148,939
PRIOR FILING DATE: 1999-08-13
PRIOR PAPLICATION NUMBER: 60/133,238
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1997-07-29
                                                                                                                                                                                                                                               NT FILING DATE: 2001-06-06
APPLICATION NUMBER: 09/565,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-07-29
PRIOR APPLICATION NUMBER: 60/040,846
PRIOR FILING DATE: 1997-03-17
                       Sequence 4, Application US/09874138
Patent No. US20020072091A1
GENERAL INFORMATION:
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US-09-884-987-2
; Sequence 2, Application US/09884987
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SOFTWARE: Patentin Ver. 2.1
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US-09-874-138-4
                                                                                        APPLICANT: Ni, Jian
US-09-874-138-4
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LENGTH: 335
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COUNTRY: US
ZIF: 20850
COMPUTER READABLE FORM:
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US-09-935-727-9
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GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REPERENCE: PF54P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/230,24
PRIOR PALLING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-11-21
PRIOR PPLICATION NUMBER: 60/252,131
PRIOR PPLICATION NUMBER: 60/252,131
PRIOR PPLICATION NUMBER: 60/215,598
PRIOR PPLICATION NUMBER: 60/218,931
PRIOR PPLICATION NUMBER: 60/18,235
PRIOR PPLICATION NUMBER: 60/146,371
PRIOR PPLICATION NUMBER: 60/131,964
PRIOR PPLICATION NUMBER: 60/131,964
PRIOR PPLICATION NUMBER: 60/131,270
PRIOR PPLICATION NUMBER: 60/124,092
PRIOR PPLICATION NUMBER: 60/121,774
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            GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu et al
TITLE OF INVENTION: DAM CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                            Length 335,
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Patent No. US20020150583A1
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4%
Matches 165; Conservative
US20020102653A1
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US-09-884-987-2
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US-09-935-727-9
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Patent No.
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QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATE:
FILING DATE: cUnknown>
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TITLE OF INVENTION: Death Domain Containing Receptor NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  Indels
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PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR RILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 9
LENGTH: 335
TYPE: PRT
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Yu, Guo-Liang
Su, Jeffrey
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 335;
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; Pred. No. 2.5e-55;
54; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox, 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
APPLICATION NUMBER: US 60/040,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HOOVET, Kenley
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 30130998504
                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-005-842-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09314889;
Publication No. US20030077694a1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
            FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                               INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acids
                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.49
Matches 165; Conservative
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sterne, Kessler, Goldstein & Fox, P.L.L.C. 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVEXNION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.8%; Score 844; DB 9; L.
49.1%; Pred. No. 1.9e-54;
Live 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                 1488.0310003/EKS/KRM
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301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
                                                                                                           PRIOR AND MARKER.

PRIOR APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
US/09/314,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                        : 202-371-2600
202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 49.19 Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not releva
MOLECULE TYPE: protein
                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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APPLICANT:
APPLICANT:
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CITY: Wa
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MEDIUM TYPE: Floppy disk
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APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                Yu, Guo-Liang
                                                                                                                                                                                                      ZIF: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                      CITY: Rockville
APPLICANT: Ni, Jian
                                                                                                                                                                                         as
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                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-756-854-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/028,711
                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 46.8%; Score 844; DB 10; Best Local Similarity 49.1%; Pred. No. 1.9e-54; Matches 164; Conservative 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1488.0310003/EKS/KRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: No. US20020009773A1 Relevant; MOLECULE TYPE: protein US-09-333-966-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AECRRILDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
                                                                                                                                                   0S/09/333,966
                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-756-854-3
; Sequence 3, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-371-2540
                         ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TIQEAKK--FARENNIKEGKIDEIMHDSIQDTAEQKVQLLL 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    APFLICATION NUMBER: US/09/756,854 FILING DATE: 10-Jan-2001 CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAWE: HOOVER, KENLEY K,
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: SINGle
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR AFPLICATION DATA: APFLICATION NUMBER: 09/095,094
                                                                                                                    STREET: 9410 Key West Avenue CITHY. Dankers.
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57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
IITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 1997-06-11
PRIOR PLICATION NUMBER: 66/052,991
PRIOR FILING DATE: 1998-06-11
PRIOR PLICATION NUMBER: 66/055,094
PRIOR PLIING DATE: 1998-06-10
PRIOR PLIING DATE: 1999-03-24
PRIOR PLIING DATE: 1999-03-24
PRIOR PLIING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3
LENGTH: 281
TYPE: PRT

CORGANISM: Homo sapiens
US - 10-041-574-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 281;
5.8e-40;
thes 97; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 5.8e
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.8%;
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Best Local Similarity 45.68
Matches 128; Conservative
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Search completed: May 9, 2003, 17:09:17 Job time : 26.3006 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 9, 2003, 17:02:31 ; Search time 28.1556 Seconds Run on:

(without alignments)
1116.509 Million cell updates/sec

1804

1 MIMIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327 US-09-446-634A-23 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* •• Database

pir2:* pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apoptosis-mediatin	Fas antiqen precur	apoptosis-mediatin	FAS soluble protei	Fas-Delta-(4,7) pr	Ψ	gene ox40 protein	B-cell activation	tumor necrosis fac		CD27 antigen precu		tumor necrosis fac	OX40 homolog - hum	tumor necrosis fac	CD27 antigen precu	nerve growth facto	B cell-associated	G2R protein - vari	hypothetical prote	·	nerve growth facto	CD30 antigen precu	tumor necrosis fac	nerve growth facto	trophozoite cystei		U	gene murine tumour
SUMMARIES	Ω	A46484	JC2395	A40036	137383	S58662	S12783	148700	A60771	GQHUT1	GQMST1	A46517	154182	GQRTT1	137552	JC4302	A49053	JN000E	A46476	D72175	T28623	D36858	A26431	A42086	A35356	COHON	C42125	T25933	JC5486	I48854
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dР	Query Match	100.0	58.7	47.5	44.9	16.9	11.3	11.2	10.8	10.5	10.3	10.1	10.0	9.9	9.5	9.4	9.3	9.5	9.1	9.1		0.6	•		8.2	7.8	•	•	7.0	8 9
	Score	1804	1058.5	856	810.5	305.5	203.5	_	٠	189.5	185	183	179.5	179	171	169	16	165.5	165	165	163	163	154.5	154.5	148	141	135.5	126.5	12	123.5
	Result No.	1	0	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	. 22	23	24	25	56	27	28	29

lymphocyte activat	FAS soluble protei	hypothetical prote	tumor necrosis fac	hypothetical prote	protein T22A3.8 [1	laminin alpha chai	T2 protein - rabbi	laminin alpha-1 ch	hypothetical prote	laminin alpha-4 ch	hypothetical prote	probable laminin a	cysteine rich prot	vacuolar sorting r	Delta-4 protein -	
138426	137384	T26972	B38634	T23064	F87908	T43291	B43692	S18253	T27283	096898	T23433	T37316	T42017	T04895	JC7569	
7	~	~	~	7	7	~	7	~	7	-	N	~	7	7	7	
255	103	1111	474	2823	2823	3102	325	3712	1620	1816	3672	3704	1274	626	989	
6.8	9.9	6.7	9.9	9.9	9.9	9.9	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	
122.5	122	120.5	119.5	119	119	119	116.5	. 116	115.5	115.5	115.5	115.5	115	114	114	
30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 A46484 apoptosis-mediating membrane-associated polypeptide Fas - mouse C;Species: Mus musculus (house mouse)
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C; Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N. J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the m A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Accession: A40484 A;Status: preliminary A;Molecule type: mRNA
A;Residues: 1-327 <wat> A;Cross-references: GB:M83649; NID:9193225; PIDN:AAA37593.1; PID:9193226</wat>
A;Experimental source: BAM3 macrophage cell line A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A; Title: Aberrant transcription caused by the insertion of an early transpos A; Reference number: A47254; MUID:93189576; PMID:7680478
A; Accession: A47254
A; Molecule type: nuclaic acid A: Residues: 1-96 <ada></ada>
A; Cross-references: GB:S56490; NID:9298505; PIDN:AAB25700.1; PID:9298506
A; Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCSInperfamily: NGF recented from homelogy
C; Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <ngf> F;81-124/Domain: NGF receptor repeat homology <ng4></ng4></ngf>
Query Match 100.0%; Score 1804; DB 2; Length 327;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps

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NCBIN: 126

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G.; Jenk nouse Fas 21-Jul-2000

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R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mem A;Reference number: A38142; MUID:92268122; PMID:1375228
                                                                                                                                                                        surface antigen Fas can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:X63717; NID:928741; PID:928742; Dehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.;
                                                                                     Ritch, N.; Yonehara, S.; Ishli, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas A;Reference number: A40036; MUID:91309137; PMID:1713127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 QPCQPGKKKVEDCKMNGGIPTCAPCIEGKEYMDKNHYADKCRRCTLCDEEHGLEVEINCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTĄTSNTNCRKQSPRNRLWLLTIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410 R:Krammer, P.H. submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLWIWAVLPLVLAG----SQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK
                         C.Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-134, 'Q',136-335 < OEH>
A; Experimental source: SKW6.4 cells
A; Note: sequence extracted from NCBI backbone (NCBIP:103810)
A; Note: in NCBI backbone the source is designated as mouse
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: GDB:132671; OMIM:134637
A; Map position: 10424.1-10424.1
C; Superfamily: NGF receptor repeat homology
C; Keyvords: apoptosis; surface antigen; transmembrane protein
F; 1-16/Domain: signal sequence #status predicted <SIG>F; 174-190/Domain: transmembrane #status predicted <TMM>F; 174-190/Domain: TMM>F; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary; not compared with conceptual translation
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49.4%; Pred. No. 4.8e-54;
tive 54; Mismatches 107
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                                                            C; Accession: A40036; S24543; A38142
   C; Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S24543
A; Accession: S24543
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-335 < KRA>
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FAS soluble protein - human
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Matches 165; Conserva
                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-335 <ITO>
                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                    A; Accession: A40036
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Best Local 3
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A; Accession: PC22A6
A; Accession: PC22A6
A; Molecule type: mRNA
A; Residues: 1-62, RFT* (KIZ)
A; Resperimental source: DBB:D2613; NID:9468488; PIDN:BAA05109.1; PID:d1005651; PID:9468489
A; Experimental source: DBB:D26113; NID:9468488; PIDN:BAA05109.1; PID:d1005651; PID:9468489
A; Experimental source: Liver
C; Genetics:
A; Introns: 62/1
C; Superfamily: NGF receptor repeat homology
C; Keywords: transmembrane protein
F; 1-21/Domain: signal sequence *status predicted <MAT>
F; 22-324/Product: Fas antigen *status predicted <MAT>
F; 44-79/Domain: NGF receptor repeat homology <MG4>
F; 81-124/Domain: NGF receptor repeat homology <MG4>
F; 11-188/Domain: NGF receptor repeat homology <MG4>
F; 11-188/Domain: NGF receptor repeat homology <MG4>
F; 11-188/Domain: Transmembrane *status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                             C; Species: Rattus norregicus (Norway rat)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C; Date: 20-Feb-1995; #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C; Accession: JC2395; PC2246
R; Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Blophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat live
A;Reference number: JC2395; MUID:94128114; PMID:7507668
241 ARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRTLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
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AEEIQAMVWEDHENSISNSRNENEGGSLE 324
                                                                                                                                                        KFQDMVQKDLGKSTPDTGNENEGQCLE
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Gaps

C.Species: Homo Sapiens (man) C.Bate: 02-3u1-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000 C.Accession: 173787	OY 57 QPCQPGKKKVEDCKANGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEBHGLEVET 113
R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G. J. Immunol. 154. 2706-2713. 1995	ARDCTVNGDEPDCVPCQEGKEYTDKAHFSS
A,Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are A,Reference number: 137383; MUID:95181785; PMID:7533181	114
A;Accession: 13/383 A;Status: preliminary; translated from GB/EMBL/DDBJ	Db 121 AHSPATPSAKRK-DPDLTWGGFVFFFC 146
A; Residues: 1-314 <res> A:Cross-references: EMBL:247993; NID:g728578; PIDN:CAA88031.1; PID:g695539</res>	
atch 44.9%; Score 810.5; DB 2; Length 314; cal Similarity 46.8%; Pred. No. 8.1e-51;	OX40 antigen precursor - rat N;Alternate names: nerve growth factor receptor homolog C;Species: Rattus norvegicus (Norway rat)
Matches 156; Conservative 50; Mismatches 100; Indels 27; Gaps 3; Ov 1 MIMIMANIPLYIAGGOIBVHHOGENSTERSTREEDENDENDENDED FOR	C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999 C; Accession: 512783; S08036 Procession: 5127845; S08036 Procession: 5127845
:	EMBO J. 9, 1063-1068, 1990 A.Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lympho
QY 57 QPCQPGKKKVEDCKANGGTPTCAPCTEGKEYADKNHYADKCRRCTLCDEEHGLEVETNCT 116 : : :	A;Reference fulliber: S1z/03; MUID:9Uz14014; FMID:413/331 A;Accession: S12783 A;Molecule type: mRNA A:Residues: 1-271 <mal></mal>
QY 117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL 176	A;Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831 C;Superfamily: Ct27 antigen; NGF receptor repeat homology C;Keywords: growth factor receptor; transmembrane protein
177 VLLIPLVFIYRYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMT	F; 1.7-Domain: slyna: Sequence *Sector's predicted <315. F; 20-271/Product: OX40 antigen #status predicted <mat> F; 211-235/Domain: transmembrane #status predicted <tmm></tmm></mat>
Db 169VRRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVMT 220	Query Match 11.3%; Score 203.5; DB 2; Length 271; Rest Local Similarity 24.4%; Dred No. 1 Ga.07.
234 IQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKA	ecc. Local Samilarity 24.4%; Figu. NO. 1.35-0/; Matches 64; Conservative 27; Mismatches 82; Indels 89; Ga
DD 221 LSQVKGEVRKNGVNEAKIDEIKNDNVQDTAEGRVQLLRNWHQLHGKKEAYDTLIKDLKKA 280 Qy 294 ECRRTLDKFQDMVQKDLGKSTPDTGNENGQCL 326	QY 2 LWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPC 59 :::
~	QY 60 QPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQ 119
RESULT 5 S5862 2 Portein - human	Qy 120 NTKCKCEPDFYCDSPGCEHCVRCASCEHGTLEPCTAT 156
C.Species: Homo Sapiens (man) C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 01-Dec-2000	99 DIVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWINCTLSGKQIRHPASNS
C;Accession: S5866; S57566 R;Liu, C.; Cheng, J.; Mountz, J.D. Blochem. J. 310, 957-963, 1995	QY 157 SNTNCREQS175 QY 157 SNTNCREQS175 1
A;Title: Differential expression of human Fas mRNA species upon peripheral blood mononud A;Reference number: 558662; MUID:96013198; PMID:7575433	176 -LVILIFLVEIYRKYRKRKCWK 196
A;Status: 33002 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A:Residues: 1-149	Db 219 GLGLLAFLTVLLALXLRKAWR 240
R.Schatzlein, C.B. submitted to the EMBL Data Library, June 1995	RESULT 7 I48700
A;Reference number: S57565 A;Accession: S57566	gene ox40 protein - mouse N.Alternate names: OX40 antigen
A; Molecule type: mRNA A; Residues: 1-132 <sch> A; Cross-references: EMBL: X89101; NID:9887457; PID:9887458</sch>	C:Species: Mus musculus (house mouse) C;Date: 02-Jul-11996 *Requence_revision 02-Jul-1996 *text_change 11-Jan-2000 C;Accession: 148700; 148334; S34377 R;Calderhead, D.N.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.
arcernad h similar	J. Immunol. 151, 5261-5271, 1993 A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell A:Reference number: 148700; MUID:94044750; PMID:8228223
Matches 63; Conservative 20; Mismatches 47; Indels 17; Ga	A.A.C.ESJUN: 148/UO A.Status: translated from GB/EMBL/DDBJ A.Molecule type: mrNA
UY I MLWIWAYLPLVLAGSSQLKWHIQGINSISESLKLRRRVHETDKNCSECLYQGGPFCC 56	A;Residues: 1-272 <res> A:Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828 R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.</res>

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Eur. J. Immunol. 25, 926-930, 1995
A;Itle: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Gecssion: 148334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14, G',16-272 <RE2>
A;Residues: 1-14, G',16-272 <RE2>
A;Gross-references: EMBL:X85214; NID:9732818; PIDN:CAA59476.1; PID:9732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stamenkovic, I.; Clark, E.A.; Seed, B.
MBO J. 8, 1403-1410, 1989
Fittle: A B-lymphocyte activation molecule related to the nerve growth factor receptor
Reference number: S04460; MUID:89356608; PMID:2475341
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C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQNT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHGWVSRCDHTRDT-LCHPCETG-FYNEAVNY-DTCKQCTQCNHRSGSELKQNCTPTQDT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 VCRCRPGTOPRODSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AVCEDRSLLATLLWETQRPTFRPTTVQSTTVWPRTSELPSPPTLVTPEGPAFAVLLGLGL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LWINAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 21-50 cBRA>
Experimental source: Burkitt lymphoma cell line
Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VLLIPLVFIYRKYRKKCWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GLLAPLTVLLALYLLRKAWR 241
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Best Local Si
Matches 69;
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DB 2;
  10.8%; Score 194.5; DB 28.6%; Pred. No. 8.6e-07.ive 20; Mismatches 7.
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VVIPIIFGILFAILLVLVFIKKVAKK 221
                         Conservative
Query Match
Best Local Similarity
Matches 59; Conserv
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A; Residues: 1-455 <SCH>
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Lumior necrosis factor receptor 1 precursor [validated] - human

NyAlternate names: P55 tumor necrosis factor receptor; TNF receptor type 1

NyContains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding proC; Species: Homo saplens (man)

C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000

C; Accession: A38208; A34899; A34900; A36555; C36555; A38201; S12057; JT0758; A60231;

Genomics 13, Z19-224, 1992

A; Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to A; Reference number: A38208; MUID:92250049; PMID:1315717

A; Rocession: A38208

A; Molecule type: DNA

A; Residues: 1-455 FUCO>

A; Cross-references: GB:M/5864; GB:M/5865; GB:M/5866; NID:9339748; PIDN:AAA61201.1; P

R; Loctscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Les

A; Reference number: A34899; MUID:90235284; PMID:2188862

A; Molecule type: DNA

A; Reference number: A34899; MUID:90235284; PMID:2188862

A; Molecule type: DNA

A; Recession: A34899; MUID:90235284; PMID:2188862

A; Molecule type: DNA

A; Recession: A34899; MUID:90235284; PMID:2188862 A; Wolecule type: mRNA A; Residues: 1-455 <LOE> A; Residues: 1-455 <LOE> A; Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754 A; Experimental source: placenta A; Note: part of this sequence, including the amino end of the mature protein, confir. B; Schall, T.J; Lewis, M; Koller, K.J; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, Cell 61, 361-370, 1990 A; Title: Molecular cloning and expression of a receptor for human tumor necrosis fact A; Reference number: A34900; MUID:90235285; PMID:2158863 A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745 K;Himmler, A; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaler, K.; Lantz, BDNA Cell Biol. 9, 705-715, 1990 expression of human and rat tumor necrosis factor receA;Reference number: A36555; MUID:91090841; PMID:1702293 A Molecule type: protein
A;Residues: 30-38;41-53, X, 55-79, XX',82-94, 'NK'; 'XX',100-104;107-128;162-167, 'X',16
A;Residues: by protein, called tumor necrosis factor binding protein, is a solustray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of A;Reference number: A38281; MUID:91017509; PMID:2170974 ώ .; 96 KCRRCTLCDEEHGLEVETNCTLIQNTKCKCKPDFYCDSPGCEHCVRCASCEHG----- 148 136 IGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRAL 195 --SPRNRLWLL 173 37 VH-ETDKNCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYAD 95 A;Residues: 1-455 <HIM> A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756 A;Accession: C36555 53; Length 277; Indels 74;

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A; Accession: B40254
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A; Gene: GDB:125913; OMIM:191190
A; Map position: 12p13.2-12p13.2
A; Map position: 12p13.2-12p13.2
A; Map position: 12p13.2-12p13.2
A; Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C; Keywords: duplication; glycoprotein: receptor; transmembrane protein
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F; 30-211/Domain: extracellular #status predicted <EXT>
F; 41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-13 <KEM>
A;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequency A;Reference number: A60231; MUID:90292116; PMID:2113477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Wolecule type: protein
A;Rosidues: 41-43, X',45-53, X',55-57 <SEC>
A;Rosidues: 41-44, M'.; Jeffes, E.W.B.; Le
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
                                                                                                            R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The CDNA for the typ
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A; Molecule type: protein
A; Experimental source: cancer patient serum
A; Experimental source: cancer patient serum
B; Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
B; Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
A; Tile: Isolation and characterization of a tumor necrosis factor binding protein from A; Reference number: A60594; MUID:89171156; PMID:2924890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
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A; Molecule type: protein
A; Residues: 41-43, X', 45-53, 'v', 55-57, 'XK', 60 <0LS>
A; Residues: 41-43, X', 45-53, 'v', 55-57, 'XK', 60 <0LS>
A; Residuental source: renal failure patient urine
B; Engelmann, H.; Novick, D.; Wallach, D.
B Bol. Chem. 265, 1531-1356, 1990
A; Hitle: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A; Reference number: A35010; MUID: 90110215; PMID: 2153136
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Blosci. Blotechnol. Blochem. 58, 2266, 2268, 1994
A.fille: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A;Reference number: JC2404; MUID:95128033; PMID:7765720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kemper, O.; Wallach, D.
ene 134, 209-216, 1993
;Title: Cloning and partial characterization of the promoter for the human p55 tumor
;Reference number: JT0758; WUID:94085779; PMID:8262379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carboxyl ends,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224 A;Note: parts of soluble TNF binding protein 1, including its amino and R;Kemper, O.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
Experimental source: urine
                                                                                                                                                                                                                                                                      A; Reference number: S12057; MUID: 91006021; PMID: 1698610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A38258; MUID: 91062364; PMID: 2174164
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Residues: 41-45 <ENG>
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A; Residues: 1-455 <NOP>
                                                                                                                                                                                                                             form of the receptor
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                                                                                                                                                                                                                                                                                                                  A; Accession: S12057
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tumor necrosis factor receptor 1 precursor - mouse
NiAlternate names: tumor necrosis factor receptor, 55K
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C; Accession: A36634; B40254; S16677; S19021; I54552; I57826
R; Levis: M: Arritaliar L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2330-28314, 1991
A; Reference number: A38634; MUD: 91187885; PMID: 1849278
A; Rocession: A38634
A; Molecule type: mRNA
A; Residues: 1-454 < LEW
A; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991
A; Rittle: Molecular cloning and expression of the type 1 and type 2 murine receptors
A; Reference number: A40254; MUD: 91246168; PMID: 1645445
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A; Residues: 1-454 <GOZ
B; R; Rissonerghis, A.M.; Gray, P.W.; Fe
B; R; Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fe
Bur. J. Immunol. 21, 1649-1656, 1991
A; Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necr
A; Reference number: 516677; MUID: 91285014; PMID: 1647956
                                                                                                                                                                                                                                                                                                                                                                                                             11;
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F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;168-196/Domain: transmembrane #status predicted <NEM>
F;212-234/Domain: intracellular #status predicted <NEM>
F;235-45/Domain: intracellular #status predicted <INI>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 YLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKQSPRNRLWL------LTIL------196
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLY---QGGPFCCQPCQPGK 63
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A; Residues: 1-454 cABR>
A; Residues: 1-454 cABR>
A; Cross-references: EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:953579
R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A; Title: Molecular cloning and expression of the mouse Inf receptor type
A; Reference number: S19021; MUID:92039815; PMID:1657766
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A;Residues: 1-454 <ROT>
A;Cross.references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.
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                                                                                                                                                                                                                                                                                                                                  Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                              10.5%; Score 189.5; DB 1; 24.7%; Pred. No. 3.1e-06; iive 31; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 KCKPDFYCD -- SPGCEHCVRCASCEHGTLE-PCTATSNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RRODDPESRTSSRETIPMNASNLSLS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIVCGKSTPEKEGELEGTTTKPL-APNPSFS 274
                                                                                                                                                                                                                                                                                                                                                                   Local Similaricy
hes 67; Conservative
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10.1%;
36.4%;
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Matches 36; Conservative
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Immunogenetics 39, 450-451, 1994

A,Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1
A; Reference number: 154522; MUID:94245292; PMID:8188324
A; Secresion: 154532
A; Secresion: 154532
A; Secretains translated from GB/EMBL/DDBJ
A; Wolecule type: mRNA
A; Residues: 1-454 <-RESA
A; Cross-references: GB:1.26349; NID:9430732; PIDN:AAA59361.1; PID:9430733
A; Cross-references: GB:1.26349; NID:9430732; PIDN:AAA59361.1; PID:9430733
B; Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
A; Title: Genomic organization and promoter function of the murine tumor necrosis factor
A; Reference number: 157826; MUID:93156721; PMID:8381516
A; Reference number: 157826; MUID:93156721; PMID:8381516
A; Retains preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-393, G', 1395-444 <-REZA
A; Residues: 1-393, G', 1395-444 <-REZA
A; Residues: 1-393, G', 1395-444 <-REZA
A; Gone type: DNA
A; Residues: 1-393, G', 1395-444 <-REZA
A; Cross-references: GB:N76565; NID:9202100; PIDN:AAA40465.1; PID:9202102
C; Gonment: This protein is one of two distantly related receptors for both TNF-alpha (cannot sense the companies of t
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CD27 antigen precursor - human
C) Alternate names: CD27L receptor; T cell activation antigen CD27
C; Species: Homo saplens (man)
C; Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C; Accession: A46517, A46454
N. A.; Gravestein, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.
J. Immunol. 149, 3937-3943, 1992
A; Fitle: Genomic organization and chromosomal localization of the human CD27 gene.
A; Reference number: A46517; MUID:93094588; PMID:1334106
A; Reference number: A6517
A; Status: not compared with conceptual translation
A; Residuas: 1-260 < LOEP
A; Molecule type: DNA
A; Residuas: 1-260 < LOEP
A; Note: sequence extracted from NCBI backbone (NCBIP:120386)
A; Note: authors propose an alternative repeat pattern
B; Camerini, D:; Walz, G; Loenen, W.A.; Borst, J.; Seed, B.
A; Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumo
A; Reference number: A46454; MUID:92013149; PMID:1655907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nerve growth factor/tumon
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F:236-454/Domain: intracellular #status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 KKVEDCKMNGGTPICAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLIQNTKC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;127-167/Domain: NGF receptor repeat homology <NG3>F;168-204/Domain: NGF receptor repeat homology <NG4>
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Matches 47; Conserv
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A Map position: 12013-12013
A Introns: 46/1; 90/1; 150/1; 180/1; 220/1
A Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface
E; 21-26/Pomain: signal sequence #status predicted <AINTS
E; 21-31/Domain: extracellular #status predicted <AINTS
E; 21-31/Domain: NGF receptor repeat homology <NGIS
E; 25-63/Domain: NGF receptor repeat homology <NGIS
E; 25-105/Domain: NGF receptor repeat homology <NGIS
E; 21-188/Region: proline/serine/threonine-rich
E; 121-188/Region: proline/serine/threonine-rich
E; 132-21/Domain: transmembrane #status predicted <TMN>
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Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
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A;Molecule type: mRNA
A;Residues: 1-58,'A',60-260 <CAM>
A;Residues: 1-58,'A',60-260 <CAM>
A;Cross-references: GB:M63928; NID:g180084; PIDN:AAA58411.1; PID:g180085
A;Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)
C;Comment: A soluble CD27 found in serum and urine is formed by proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: 154182
B;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
A;Fite: Construction and evaluation of a hncDNA library of human 12p transc A;Reference number: 154182; MUID:93252381; PMID:8486360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 KNCSEGLYQG-GPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVET 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 ICCSRCPPGTYVSAKCSRIRDT-VCATCAE-NSYNEHWNYLTICQLCRPCDPVMGLEEIA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CEH-GTLE--PCTATSNTNCR---KQSPRNRLWLLTILVLLIPL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLWIWAVL-----PLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 KSCPERHYWAQGKLCCOMCEPGTFLVKDCDQHRKTAQCDPCIPGVSFSPDHHTRPHCESC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 NCTLTQNTKCKCKPDFYCDS-------PGCE------HCVRCAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;212-260/Domain: intracellular *status pression (*) F;95/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor receptor 2-related protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-211/Domain: transmembrane #status predicted <TMN>
(2-260/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TLCDEEHGLEVETNCTLTQNTKCKCKPDFYCDSPGCEHC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
10.0%; Score 179.5; DB 2;
Best Local Similarity 25.5%; Pred. No. 1.5e-05;
Matches 65; Conservative 27; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 183; DB 1;
; Pred. No. 5.4e-06;
11; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-435 <RES>
                                                                                                                                                                                                                                       A;Cross references: GDB:132582; OMIM:186711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:1230195; OMIM:600979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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27.5%; Pred. No. +ive 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: kidney cell line C; Genetics:
          Best Local Similarity 27.59
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-7 <:SU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May Job time: 30.1556 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-461 <SUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: PC4093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: tnfr
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                                                                                                            å
                                                                                                                                                                                                                                                                                                                    tumor necrosis factor receptor 1 precursor - rat

Uncontains: tumor necrosis factor binding protein 1 (TNF blocking factor)

C; Species: Rattus norvegicus (Norway rat)

C; Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999

C; Accession: B36555

R; Himmler, A: Maurer-Fogy, I: Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;

DNA Cell Biol. 9 705-715, 1990

A; Title: Molecular cloning and expression of human and rat tumor necrosis factor receptc

A; Reference number: A36555; MUD:91090841; PMID:1702293

A; Molecule type: mRNA

A; Residues: 1-461 < HINA

A; Cross-references: GB:M63122; NID:9207361; PIDN:AAA42256.1; PID:9207362

C; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C; Superfamily: tumor necrosis factor receptor; transmembrane protein

F; 1-29/Domain: signal sequence #status predicted < SIG>
F; 30-201/Product: tumor necrosis factor receptor type 1 #status predicted < MAT>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor receptor type 1 #status predicted < TBP>
F; 30-201/Product: tumor necrosis factor propeat homology < NG3>
F; 84-126/Domain: NGF receptor repeat homology < NG3>
F; 86-126/Domain: NGF receptor repeat ho
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OX40 homolog - human
C;Species: Home sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: 137552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Bur. J. Immunol. 24, 677-683, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The human OX40 homolog: CDNA structure, expression and chromosomal assignment A;Reference number: 137552; MUID:94170844; PMID:7510240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΄.
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F:235-461/Domain: intracellular #status predicted <INT>
F:54,151;201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
          175 FQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLMLAVLLPL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 KKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETN-CTLTQNTK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YLVSDCPSPGQETVCEVCDKGTFTASQNH-VRQCLSCKTCRKEM-FQVEISPCKADMDTV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 179; DB 1; Length 461; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 CGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKEKQNTVC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKCKPDFYCDSPGCEH--CVRCASCEHGTLE-PCTATSNTNC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: 137552
A;Status: prellminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.2 les 49; Conservative
                                                                                                     183 VFIYRKYRKRC-WK 196
                                                                                                                                                                      235 AFFLLLATVFSCIWK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor A;Reference numbér: JC4302; WJID:96011645; PMID:7590278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
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                                                                                                                                                                                                                   96 -KCRRCTLCDEEHGLEVEINCTLTQNTKCKC------KPDFYC-----DS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LLPLVLNALLVDVYPAGVHGLV-----LHPGDREKRESLCPQGKYSHPQNRSICCTK 61
                                                                                                                                                    27 TGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNT-VCRPCGPG-----FYNDVVSS 78
                                                                                         40 IDKNCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYAD----
                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 ONTKCKCKCKPDFYCD--SPGCEHCVRCASCEHGTLE-PCTATSNTNCRKQS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RDTVCGCRKNOYRKYWSETLFQCLNCSLCPNGTVQLPCLEKQDTICNCHS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.4%; Score 169; DB 2; Length 461;
Local Similarity 27.1%; Pred. No. 9.2e-05;
les 46; Conservative 23; Mismatches 81; Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Domain: signal transduction #status predicted <SIT>
No. 4.1e-05;
smatches 62;
                                                                                                                                                                                                                                                                                                                                                    134 PGCEHCVRCASCEHGTLEPCTATSNTNCRKQSP 166
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Length 277;

DB 2;

Score 171;

9.58;

Query Match

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242 TLICSLRDLKMRTAADKIE 260

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Best Local S
Matches 91
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bridgham J.T., Johnson A.L.;
"Fas Expression and Regulation in Hen Granulosa Cells.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF296874; AAG02242.1;
HSSP; O14763; 1D4V.
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                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9031;
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                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 LVLLIPLVFIYRKYRKRKCWKRRQD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                       182
           285
                                                                                           124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLWIWAVLPLYLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-LLIPIVLGLRRYKKHRDGKHGYD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKCRCKSNFFCNALKCEHCDPCTMCEHGIIEECTQTSNTKCKEKGSTTGSKHHFLWLLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEVETDCTTIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTGIWVLLPLIL-----TCIAGSLSTSINDCKIKNETQYSTG---YLSGNFCCQLCP
DLIKGLKKAECRRTLDKFQ 303
                                   VPDIVREMTLEQXMTFVRHHRLSEPTIXETLLDNXNNTSEQKIKLFQKWYQKHGMGGAYE
                                                                                          ATTVVFVTLAVAAGLIFYFK--RKVNNYTTQGNTAAADTGKVHSPETLRLTHIDVDLTHH
                                                                                                          TILVLLI-----PLYFIYRKYRKKCWKRRQDDPESRTS---SRETIPMNASNLSLSKY 224
                                                                                                                                                CTSTENAECSCAKNHYCNSSRCEHCESCTVCENGQIEKECTSTSDTVCRMQEAGMPPWGT 123
                                                                                                                                                               CTLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLE-PCTATSNTNCRKQSPRNRLWLL
                                                                                                                                                                                                    CCTKCKRGHVKSIDCPKT--QAHCVPRKSGEEYMDHINDLDECMRCRSCDKALGLEVVKN 63
                                                                                                                                                                                                                              CCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETN 114
                                                                 IPRIAEDMTIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQ
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                     PS50017; DEATH_DOMAIN; 1
PS00652; TNFR_NGFR_1; UN
PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (TrEMBLrel. 16, 1 (TrEMBLrel. 16, 1 (TrEMBLrel. 19, 1 (TrEMBLrel. 19, n (Fragment).
                                                                                                                                                                                                                                                                                                             312 AA; 35275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                    24.3%; Score 438;
35.1%; Pred. No. (
                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.
                                                                                                                                                                                                                                                                                                             5496BCF1E4CE676C
                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                    6.8e-31;
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                                                                                                                                                                                                                                                           108;
                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                   Length 312;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phasianinae;
                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                          Gaps
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Search completed: May 9, Job time: 29.6495 secs

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Best Local S
Matches 86
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Q9DGH7;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bridgham J.T., Johnson A.L.;
"Fas Expression and Regulation in Hen Granulosa Cells.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF296875; AAG02243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2002 (TrEMBLrel. 20,
Fas ligand receptor soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFF; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TNFK_NGFR_1; UNK
PROSITE; PS50050; TNFK_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00531; death; 1. Pfam; PF00020; TNFR_c6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; 014763; 1D4V
                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
224
                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CCTKCKRGHVKSIDCPKT--QEHCVPCKCGEEYMDHINDLDECMRCRSCDKALGLEVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCQPCQPGKKKVEDCKMNGGTFTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETN 114
                                                                                                                                                                                                                                                                                      TILVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMT
                                                                                                                                                                                                                                                                                                                                                   CTSTENAECSCAKNHYCNSSRCEHCESCTVCENGQIEKECTSTSDTVCRMQ-----
                                                                                                                                                                                                                                                                                                                                                                                  CTLIQNIKCKCKPDFYCDSPGCEHCVRCASCEHGILE-PCTAISNINCRKQSPRNRLWLL 173
                                                                                                                                                                  IQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKA
KMRTAADKIE
                                                       ECRRTLDKFQ 303
                                                                                                           LEQVMTFVRHHRLSEPTIEETLLDNSNNTSEQKIKLFQKWYQKHGMGGAYETLICSLRDL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                               285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
32431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
form (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 428.5; DB 13;
Pred. No. 4.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_1
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A9761960CCD79E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                114
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Fas receptor (Fragment).
Rattus norvėgicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQNTKCKC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQPGKKK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=WISTAR; TISSUE=CORPUS LUTEUM;
Lareu R.R., Dharmarajan A.;
"Cloning and expression of Fas and Fas Ligand in the apoptotic rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fas antigen spliced variant.
Oryctolagus culculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
ISONO T., Tanbe Y., Nagano Y., Seto A.;
ISONO T., Tanbe Y., Nagano Y., Seto A.;
Splicing and allelic variation in the rabbit Fas antigen (Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB021297; BAA78429.1;
HSSP; O14763; IDAV.
InterPro; IPR001368; TWFR_C6.
Pfam; PF00020; TWFR_C6; 3.
SWART; SM00208; TWFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 609.5; DB 11; Length
69.3%; Pred. No. 1.7e-46;
Live 16; Mismatches 29; Indels
                                                                                                                                                                                                                                            corpus luteum ";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF104031, AAD20221.1;
HSSP; P25942; 1CDF.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR.C6; 2.
SMART; SM00208; TNFR. 2.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       150 150
150 Aa; 16644 MW; 7DEC76EC40A6BA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0552; TWFR MGFR_1; UNKNOWN_1.
PROSITE; PSSO050; TWFR_NGFR_2; 2.
SEQUENCE 263 AA; 30374 MW; 6D76782ADEDIBFD7 CRC64;
                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 KPDFYCDSPGCEHCVRCASCE-HGTLEPCT 154
                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
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Q9XS60;
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Q9XS60
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56 COPCOPCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNKLWLLTI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 -----VVIKKPCRKHR--KENQGPHESTTLNPET-AINLSDVDLSKYITTIAGAMTLS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 LVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 EAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAEC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLWIWAVLPLVLAGSQLR----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca arctoides (Stump-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;

Cloning of fas gene in stump-tailed monkey.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF332357; AAG49394.1;

HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.6%; Score 768; DB 6; Length 31, 47.6%; Pred. No. 3.2e-60; Live 41; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000488; Death.
Interpro; IPR001368; TWFR_c6.
Ffam; PF00531; Geath; 1.
Ffam; PF00532; TRFR_c6; 2.
SWART; SW00005; DEATH; 1.
SWART; SW00208; TRFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50052; TWFR_NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_1; 1.
SEQUENCE 310 AA; 34806 MW; C5C79BF1F804A419 CRC64;
                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fas antigen APO-1/CD95.
                                                      294 ECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                              150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 RRTLDKFQDMVQKDLGKSTPDTGNENEG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTLAEKIHAVILKDI---TSDTENSNFG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
42.6%;
Best Local Similarity 47.6%;
Matches 156; Conservative 4
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca
NCBI_TaxID=9540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                           01-MAR-2001
01-DEC-2001
                                                                                                                                                                              Q9GK28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R230
Q9R230;
                                                                                                                                        RESULT 11
09GK28
AC 09GK28
DT 01-MP
DT 01-DE
DE FAS 8
GN MACCO.
OC BUKAI
OC BUKAI
OC CETCO.
OX (1)
RP SEQUE
RA (1)
RP SEQUE
DR INTEX
DR PÉRMI,
DR PROSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
Q9R230
ID Q9R230
AC Q9R230
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Gaps

Gaps 17; Length 263; Indels Query Match 28.9%; Score 520.5; DB 6; Best Local Similarity 48.8%; Pred. No. 2.6e-38; Matches 100; Conservative 27; Mismatches 61;

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CTLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCR-KQSPRNRLWLL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 IQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Σ
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                                                                                                                                                                          239 SQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQPLRNWYQLHGKKDACDTLIKGLKTAD 298
                                                235 QEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
60 RNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGHLSSKCRRCRLCDEGHGLEVEINC 119
                                                                                           175 ILVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazo, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWIWAVLPLVLAGSQL----RVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 TILVILIPLVEIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onnma
                             116 TLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRL-WLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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44.5%; Score 802; DB 6; Length 32.
Best Local Similarity 47.7%; Pred. No. 3.2e-63;
Matches 159; Conservative 48; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
TISSUE=LYMPHOCYTE;
Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto
"Cloning of sheep fas antigen.";
Submitted (MRR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011671; BAA37093.1;
HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCFEE844B2BE387A CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       327
                                                                                                                                                                                                                          295 CRRTLDKFQDMVQKDLGKSTPDTGNENEG 323
                                                                                                                                                                                                                                              299 LCTLAEKIHAVILKDI---TSDTENSNFG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSF; #23.42.

INTERPRO; IPR001368; Death.
INTERPRO; IPR001368; TNFR_C6.
Pfam; PF00531; death; 1.
SMART; SM0005; TNFR_C6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS50017; DEATH, 1.
PROSITE; PS50052; TNFR, MGFR_1; 1.
PROSITE; PS50050; TNFR, MGFR_1; 1.
PROSITE; PS50050; TNFR, MGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                       PRT;
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10,
17,
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01-MAY-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                       Fas protein.
                                                                                                                                                                                                                                                                                                                                    097491
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                                                                                                                                                                                                                                                                                                                  CQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNC 115
                                                                                                                                                                                                                                                60 RNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGHFSSKCRRCRLCDEGHGLEVEINC 119
                                                                                                                                                                                                                               TLIQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTAISNINCRKQSPR-NRLWLLT 174
                                                                                                                                                                                                                                                                                                                                                          MTIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLWIWAVLPLVLAGSQLR----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC 55
                                                                                                   1 MLWIWAVLPLVLAGSQLR-----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca assamensis (Assam's macaque) (Assam's monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                     175 ILVLLI---PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                       14;
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49.2%; Pred. No. 2.9e-63;
ive 45; Mismatches 111; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 334;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE58DB046C67834F CRC64;
      37531 MW; 2DC5B1661C3191C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                   46; Mismatches 108;
                                      45.2%; Score 815; DB 6;
49.4%; Pred. No. 2.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       292 KAECRRILDKFQDMVQKDLGKSTPDTGNENEG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPO, IPRO00488; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00531; death; 1.
Pfam; PF00050; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00502; TNFR, 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                      Best Local Similarity 49.4 Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas antigen APO-1/CD95
           A);
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         334
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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           SEQUENCE
                                       Query Match
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                                                                                                                                                                                                                        61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                     121 TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQ-----SPRNRLWLLTI 175
                                                                                                                                                                                                                                                                         176 LVILIPLVFIYRKYRKRKKGWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQ 235
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                               EAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAEC 295
                                                                                                                                                                                               | || :|||:|
| MTGIWVLPLIL-----TCIAGSLSTSINDCKIKNETQYSTG---YLSGNFCCQLCP 49
                                                                                                                                                                                                                                                                                                                                                    1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDRNCSEGLYQGGPFCCQPCQ 60
          gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonhuman primate
Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21383618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                       98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FAS antigen CD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, sequencing, and homology analysis of non Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
EMBL; AF344843; AAR37602.1; -...
HSSP; P55445; ldd.
InterPro; IPR000488; Death.
InterPro; IPR001368; TWFR_c6.
Pfam; PF0023; death; 1.
Pfam; PF0020; TWFR_c6; 2.
SWART; SW00005; DEATH; 1.
                                                                                                                                                 45.5%; Score 820; DB 6;
49.4%; Pred. No. 7.8e-65;
tive 44; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                             296 RRTLDKFQDMVQKDLGKSTPDTGN----ENEGQCL 326
                                                                                                                                                                                                                                                                                                                                                                                        286 CALAEKIQDIVQKDI---TSDHDNLDIRDEKERQSL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                        Best Local Similarity 49.4%
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_Tax:ID=9531;
                                                                                                                                                Query Match
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56 CQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNC 115
                                                                                                                                                                                                                                                                                                                                                                                 60 RNPCPPGERKARDCIVNEDEPDCVPCQEGKEYIDKGHFSSKCRRCRLCDEGHGLEVEINC 119
                                                                                                                                                                                                                                                                                                                                                                                                                             116 TLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPR-NRLWLLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                               175 ILVILLPEVETYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 QEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWIWAVLPLVLAGSQLR----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A SEQUENCE FROM N.A.

A Shui B., Chi L., Zhang Y.R.;

T "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";

Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";

EMBL, AY007572, AAG16762.1;

REMBL, AY007572, AAG16762.1;

REMBL, AY007672, TNFC.6:

REMBL, AY007672, TNFC.6:

REMBL, AY007672, TNFC.6:

REMBL, AY007672, TNFC.6:

REMBL, AY007631;

REMBL, 1.

REMBL, CONOMINER, DEATH, 1.

REMBL, SMOOMOS, DEATH, 1.

RAMART, SMOOMOS, DEATH, 1.

SMART; SMOOMOS, DEATH, 1.

RAMART; SMOOMOS, TNFR, 2.

REMBL, SMOOMS, TNFR, 2.

REMBL, SMOOMS, TNFR, 2.

REMBL, SMOOMS, TNFR, 3.

REMBL, SMOOMS, TNFR, MGFR, 3.

REMBL, SMOOMS, TNFR, MGFR, 3.
                                                                                                                                                                                                                                             Length 331;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                          1D843C4DE1D343F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fas antigen.
                                                                                                                                                                                                                                 Query Match 45.3%; Score 816.5; DB 6; Best Local Similarity 49.5%; Pred. No. 1.7e-64; Matches 163; Conservative 46; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 CRRTLDKFODMVQKDLGKSTPDTGNENEG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 LCTLAEKTHAVILKDI---TSDTENSNFG 324
                                             PRT;
PS$0017; DEATH_DOMAIN; 1
PS$00652; TNFR_NGFR_1; 1.
PS$0050; TNFR_NGFR_2; 2.
                                                                                                                                     95
282
298
300
37277 MW;
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NCBI_TaxID=9544;
                                                                                                                                                      VARIANT
VARIANT
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SEQUENCE
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VARIANT
                            PROSITE
                                             /ARIANT
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56 COPCOPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNC 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 TLIQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPR-NRLWLLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIWIWAVLPLVLAGSQLR----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ILVLLI--PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-type Fas antigen.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                 nonhuman primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 333;
                                                                                                                           MEDLINE-21383618; Pubmed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.
Welss W.R., Ansari A.A.;
Craniata; Vertebrata; Eutele
Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98C17F766762F287 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                 Welss W. K., Ansarl A.A.;
Welss W. K., Ansarl A.A.;
"Cloning, sequencing, and homology analysis of non-
Fas/Fas-ligand and co.stimulatory molecules.";
Immunogenetics 53:315-328(2001).
EMBL: A544483; AAK37529.1;
HSSP: P25445; lDDF.
InterPro: IPR001369; TNFR_C6.
Pfam: PF00021; death.
Pfam: PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
Pfam: PF00021; DEATH; 2.
RAPERIS PS0005; TNFR_NGFR_1; 1.
RROSITE; PS00052; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.6%; Score 822.5; DB 6;
49.8%; Pred. No. 4.9e-65;
ive 47; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 AECRRILDKFQDMVQKDLGKSTPDTGNENEG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Isono T., Tanbe Y., Nagano Y., Seto A.;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 RNPCPPGERKARDCIVNEDEPDCVPCQEGKEYIDKGHFSSKCRRCRLCDEGHGLEVEINC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQKVQLIRNWYQLHGKKDACDTLIKGLKTAD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLTQNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRL-WLLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ILVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 QEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLWIWAVLPLVLAGSQLR-----VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunosenetics 53:315-328(2001). EMBL: AF34485) AAK37610.1; -. HSSP: P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.8%; Score 825.5; DB 6; Length 331; 49.8%; Pred. No. 2.7e-65; Live 46; Mismatches 108; Indels 11.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21383618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FAS antigen CD95.
Macaca mulatta (Rhesus macaque).
                                                                                                      (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                             331 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 LCTLAEKIHAVILKDI---TSDTENSNFG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                        Cercopithecinae; Macaca
NCBI_TaxID=9545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                          FAS antigen CD95.
                                                                                                    01-JUN-2001 (
01-JUN-2001 (
01-JUN-2002 (
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Matches 164;
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Q9BDP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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WEDLINE-20237686; PubMed-10773350;

WA MILAYARMA Y. Terao K. Inoue-Murayama M.;

"Molecular Cloning and characterization of cynomolgus monkey Fas.";

"Mulayama Y. Terao K. Inoue-Murayama M.;

"Molecular Cloning and characterization of cynomolgus monkey Fas.";

"Molecular Cloning and characterization of cynomolgus monkey Fas.";

"Manunol. 61:474-485(2000)

"NE REBL!, AB031420; BaA83551.1;

"NE HSSP; P25445; IDDP.

"NE HSSP; P25445; IDDP.
"NE REPROST: About Ab
                                                                                                                        TÜNTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPR-NRLWLLTIL 176
                                                                                                                                                                                                                                 236 EAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAEC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPCOPCKKKVEDCKMNGGIPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVEINC 115
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177 VILIP-LVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQ
                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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49.7%; Pred. No. 3.8e-66;
Live 47; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Death receptor Fas (APO-1/CD95).
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Best Local Similarity 49.7%
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9TSN4
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QEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAE 294
                                                                                                                       ILVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQ-----SPRNRLWLLTI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLWIWAVI.PLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Janbe Y., Magano Y., Seto A.;

"Splicing and allelic variation in the rabbit Fas antigen gene.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; ABO21299; BAA78431.1;

HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQ
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
C-type FAS antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.0%; Score 829.5; DB 6;
50.3%; Pred. No. 1.1e-65;
iive 43; Mismatches 97;
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                                                                                                                                                                                 295 CRRTLDXFQDMVQKDLGKSTPDTGNENEGQCL 326
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INTERPOS | 1PR000488; Death.
INTERPOS | 1PR001368; TNFR_C6.
Féam; PF000531; death; 1.
SMARY; SM00005; TNFR_C6; 3.
SMARY; SM000065; DEATH; 1.
SMARY; SM000069; TNFR; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00502; TNFR_MGFR_1; UNKNO PROSITE; PS00509; TNFR_MGFR_1; UNKNO PROSITE; PS00050; TNFR_MGFR_1; UNKNO PROSITE; PS00509; TNFR_MGFR_1; UNKNO PROSITE; PS00509; TNFR_MGFR_1; UNKNO PROSITE; PS00509; TNFR_MGFR_1; UNKNO PROSITE; PS00509; TNFR_MGFR_1; DNFNO PROSITE; PS00509; TNFR_MGFR_1; DNFNO PROSITE; PS00509; TNFR_MGFR_1; DNFNO PROSITE; PS00509; TNFR_MGFR_1; DNFNO PROSITE; PS00509; TNFR_MGFR_2; 2.
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May 9, 2003, 17:00:40 ; Search time 28.6495 Seconds (without alignments) 2351.779 Million cell updates/sec
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1 MLWIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_rvirus:* sp_bacteriap:*

sp_archeap:

sp_virus:*
sp_vertebrate:*

sp_phage:* sp_plant:* sp_rodent:*

sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*

1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*

SPTREMBL_21:*

Database :

sp_organelle:*

	Description	Q9bdp0 actus trivi	Q9tsn4 macaca fasc	Q9xs29 oryctolagus	Q9bdn0 macaca neme	Q9bdp2 macaca mula	Q9tv79 oryctolagus	Q9bdn4 cercocebus	Q9g140 macaca mula	Q9gk36 macaca assa	097491 ovis aries	Q9gk28 macaca arct	Q9r230 rattus norv	Q9xs60 oryctolagus	Q9dgh8 gallus gall	O9dqh7 qallus qall	Q8sq52 felis silve
SUMMARIES	aı	09врр0	O9TSN4	Q9XS29	ONG660	Q9BDP2	Q9TV79	Q9BDN4	Q9GL40	Q9GK36	097491	Q9GK28	Q9R230	09X860	оврен8	Q9DGH7	088052
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	Query Match Length DB	328	331	320	331	333	319	331	334	331	327	310	150	263	312	285	147
æ	Query	46.5	46.3	46.0	45.8	45.6	45.5	45.3	45.2	44.5	44.5	42.6	33.8	28.9	24.3	23.8	23.1
	Score	839.5	832	829.5	825.5	822.5	820	816.5	815	802.5	802	768	609.5	520.5	438	428.5	416
	Result No.	1		m	4	വ	9	7	8	6	10	11	12	13	14	15	16

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882051 029DF34 882049 029DF20 029DDD2 029DDD2 029DD2 029PV34 039PW79 039PW79 039PW79 039PW79 049PW79 069PW7	057121 057128 057098 057284 057284 057115 057115 057120 057120
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11112222222222222222222222222222222222	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

	Gaps
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е п	Length 328; Indels 7
PRT; 328 AA. eated) ist sequence update) ist annotation update) ist annotation update) y) (Douroucouli). Craniata; Vertebrata; Bu Platyrrhini; Cebidae; Ao Platyrrhini; Cebidae; Ao S35; A.E., King C.L., Genain 1010gy analysis of nonhuma cory molecules.";). 1. 1. 2. 2. 2. 3. -> T. B3DEDIDAC97D6353 CRC64;	DB 6; e-66; 107;
PRT; 328 AA. Created) Last sequence update) Last annotation updat key) (Douroucouli). Craniata; Vertebrat Platyrrhini; Cebida pl535; ne A.E., King C.L., G mology analysis of no atory molecules."; 01). IN; 1. IN; 1. 2; 2. S -> T. S -> T.	Score 839.5; DB 6; Pred. No. 1.5e-66; 49; Mismatches 107;
PRT; 7, Created) 7, Last sequ. 11, Last annomonkey) (Douglata; Cranian; 11491535; Mayne A.E., 1 homology ar mulatory mol 1; 1,	4
EMBLrel. 17, Crea EMBLrel. 17, Last EMBLrel. 17, Last 15. Last 16.	46.5%; 50.2%; ative
11 0 09BDP0 09BDP0 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence updat 01-JUN-2001 (TrEMBLrel. 17, Last sequence updat 01-JUN-2001 (TrEMBLrel. 17, Last sequence updat 01-JUN-2001 (TrEMBLrel. 21, Last annotation upd Rotus trivirgatus (Night monkey) (Douroucouli). Enkaryotta; Metazoa: Chordata; Cranlata; Vertebrammalla; Eutheria; Primates; Platyrrhini; Cebi NCBL_TAXID-9505; 11 12 12 13 14 15 15 16 17 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	46. Ilarity 50. Conservative
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1 MLWIWAVLPLVL---AGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQ 57

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 9, 2003, 16:58:17 ; Search time 15.3127 Seconds (without alignments) 885.720 Million cell updates/sec Run on:

Title: US-09-446-634A-23
Perfect score: 1804
Sequence: 1 MLWIWAVLPLVLAGSQLRVH......KDLGKSTPDTGNENEGQCLE 327

112892 seqs, 41476328 residues Scoring table: BLOSUM62 Gapox 10.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P25446 mus musculu	Q63199 rattus norv		077736 sus scrofa	P51867 bos taurus	Q9qzm4 mus musculu	O00220 homo sapien	mus m	٥	P15725 rattus norv	P47741 mus musculu	Q93038 h tumor nec	2 homo	P19438 homo sapien	mrs m	Q9er62 mus musculu) homo	O14763 homo sapien	rattn	P26842 homo sapien	COWPC	_		Q8uya7 camelpox vi	P41272 mus musculu		P18519 gallus gall	-	8		O19131 bos taurus	Q28203 bos taurus	095407 homo sapien
SUMMARIES	e e	TNR6_MOUSE	TNR6_RAT	TNR6_HUMAN	TNR6_PIG	TNR6_BOVIN	T10B_MOUSE	T10A_HUMAN	TR23_MOUSE	TR14_HUMAN	TNR4_RAT	TNR4_MOUSE	TR12_HUMAN	TNR5_HUMAN	TR1A_HUMAN	TR1A_MOUSE	TR22_MOUSE	TNR3_HUMAN	T10B_HUMAN	TR1A_RAT	TNR7_HUMAN	CRMB_COWPX	TNR4_HUMAN	TR1A_PIG	CRMB_CAMPS	TNR7_MOUSE	T10D_HUMAN	TR16_CHICK	TNR5_MOUSE	T10C_HUMAN	CRMB_VARV	TR1A_BOVIN	TNR5_BOVIN	TR6B_HUMAN
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	Query Match Length	327	324	335	332	323	381	468	176	283	271	272	417	. 277	455	454	180	435	440	461	260	351	277	461	349	250	386	416	289	259	349	471	269	300
æ	Query	100.0	58.7	47.5	46.6	45.1	15.1	11.9	11.4	11.4	11.3	11.2	10.9	10.8	10.5	10.3	10.1	10.0	10.0	•	6.6		٠		9.3		9.5		•			8.9		9.8
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P07174 rattus norv											
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1 TR16_F	1 TNR8_H	1 TNR3_M	1 TRIB_H	1 T11B_H	1 T11B_R	1 T11B_M	1 TR16_MC	1 TR16_HU	1 XEDA_HU	1 TR11_HC	1 VS41_G1
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ALIGNMENTS

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A madgard 2.1.

A madgard and a more explained by defects in Fas antigen that mediates apoptosis.";

A matigen that mediates apoptosis.";

L Nature 356:134-317(1992).

C -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase.8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase.8 proteolytic activation which initiates the subsequent cascade of caspasas.

C aspartate-specific cysteine proteases) mediating apoptosis. FAS-caspared apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).

C --- Subsclidura Locatron: Type I membrane protein.

C --- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS, LIVER, LUNG, HEART, AND ADULT OVARY.

C --- DOMAIN: CONTAINS A DEEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

C --- DISEASE: DEFECTS IN THRESFG ARE THE CAUSE OF A LYMPHOPROLIFERATION PROTEINS.

C --- DISEASE: DEFECTS IN THRESFG ARE THE CAUSE OF A LYMPHOPROLIFERATION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Adachi M., Watanabe-Fukunaga R., Nagata S.;
"Aberrant transcription caused by the insertion of an early
transposable element in an intron of the Fas antigen gene of lpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0050; TNFR_NGFR_2; 2.
PROSITE; PSS0017; DEATH_DOMAIN; 1.
PROSITE: PSS0017; Transmembrane; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                  Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                  Natl. Acad. Sci. U.S.A. 90:1756-1760(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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                                                                                                                                                                                                       MEDLINE-92195401; PubMed-1372394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, S56490; AAB25700.1; EMBL, S56485; AAB25700.1; JOINED. EMBL, S56486; AAB25700.1; JOINED.
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PROSITE; PS50050; TNFR_NGFR_2; 2.
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
Pfam; PP00531; death; 1.
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HSSP; P25445; 1DDF.
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SIGNAL
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                                                                                                                                                                               VARIANT LPR
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                          mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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THE HELLE IN THE PROPERTY OF T
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61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 198:666-674(1994).

-I- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or
                                                                                                                                                                                                                                                                                                                      TKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTILVLLI 180
                                                                                                                                                                                                                                                                                                                                                                          181 PLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDMTIQEAKKF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRTLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                   1 MLWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimura K., Yamamoto M., Wakatsuki T.;
"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver.";
BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
I -> N (IN LPR).
H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
YCBI_TaxID=10116;
                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                Score 1804; DB 1; Length 327; Pred. No. 1e-133; 0; Mismatches 0; Indels 0;
                                                                                                                                          -> N (IN LPR).
-> R (IN REF. 3).
FGBFFC5ACE356EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFQDMVQKDLGKSTPDTGNENEGQCLE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-94128114; Pubmed-7507668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                               100.08;
                                                                                                                                                                     37418 MW;
                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                         Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  69
78
97
1115
1123
1139
1153
161
43
114
246
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                                                                                                                                                        38
327 AA;
                                                                                                                                                                                                             Similarity
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                            DISULFID
DISULFID
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CARBOHYD
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                                                                                                                                                                                                Query Match
                                                                                                                                          VARIANT
                                                                                                                                                                                                               Local
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VARIANT ALPS PRO-241
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                both (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
SIMILARITY: CONTAINS 3 TWER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEATH.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

MA: D25D583C909D9D09 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLNIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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Pred. No. 1.4e-75;
L; Mismatches 80; Indels 7;
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TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TWIR-CYS 1.
TWIR-CYS 2.
TWIR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 2. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000488; Death.
InterPro: IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36835 MW;
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61.1%;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; D26112; BAA05108.1; -. HSSP; P25445; 1DDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00005; DEATH; 1
SMART; SM00208; TNFR; 3.
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139
154
162
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SIGNAL
CHAIN
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TRANSMEM
DOMAIN
REPEAT
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Matches
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STRUCTURE BY NMR OF 218-335.
MEDILES-97123323; Pubmed-8967952;
Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
"NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
236 KFARQHKIPESKIDEIEHNSPQDAAEQKIQLLQCWYQSHGKTGACQALIQGLRKANRCDI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-91309137; PubMed-1713127;
Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
Sameshima M., Hase A., Seto Y., Nagata S.;
"The polypertide encoded by the CDNA for human cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cascino I., Fiucci G., Papoff G., Ruberti G.; "Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced alternative splicing."; J. Immunol. 154:2706-2713(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor (FASL (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruberti G
variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen, a member of the tumor necrosis factor/nerve growth fac
receptor superfamily. Sequence identity with the Fas antigen.";
J. Biol. Chem. 267:10709-10715(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oehm A., Behrmann I., Falk W., Pavlita M., Maier G., Klas C.,
Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION MEDLINE-95181785; Pubmed-7553181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 5).
TISSUB-PETIPHERAL blood lymphocytes;
Schaetzlein C.E., Pochlmann R., Philippsen P., Eibel H.;
Subantted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eibel H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          TURG HUMAN STANDARD; PRT; 335 AA. P2445; Q14292; Q14295; Q14295; Q14292; Q16652; Q16MY-1992 (Rel. 22, Created) G1-MAY-1992 (Rel. 22, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member 6 preceptor) (Apoptosis-mediating surface antigen FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
                                                                 299 LDKFQDMVQKDLGKSTPDTGNENEGQCLE 327
                                                                                                           296 AEEIQAMVWEDHENSISNSRNENEGOSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92268122; PubMed-1375228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 156:4622-4630(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFRSF6 OR APT1 OR FAS OR FAS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fas can mediate apoptosis.
Cell 66:233-243(1991).
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VARIANTS ALPS ASP-257 AND SER-310.
MEDLINE-97180739; PubMed-9028957;
Sneller M.C., Wang J., Dale J.K., Strober W., Middelton L.A., Choi Y.,
Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-99192146; PubMed-1000885;
Jackson C.E., Fischer R.E., Hau A.P., Anderson S.M., Choi Y., Wang J.,
Dale J.K., Fleisher T.A., Middelton L.A., Sneller M.C., Lenardo M.J.,
Straus S.E., Puck J.M.;
"Autoimmune lymphoproliferative syndrome with defective Fas: genotype
MEDLINE=95300225; PubMed=7540117; Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A., Lin A.Y., Strober W., Lenardo M.J., Puck J.M.; Dominant interfering Fas gene mutations impair apoptosis in a human autoinmune lymphoproliferative syndrome."; Cell 81:935-946(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lenardo M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT ALPS ALA-28.
MEDLINE-97463833; PubMed-9322534;
Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Fas/Apol mutations and autoimmune lymphoproliferative syndrome in patient with type 2 autoimmune hepatitis."; Gastroenterology 113:1384-1389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99038860, PubMed-9821419, Infante A.J., Britton H.A., DeNapoli T., Middelton L.A., Lenardo M. Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.; "The clinical spectrum in a large kindred with autoimmune lymphoproliferative syndrome caused by a Fas mutation that impairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Clincial, immunologic, and genetic features of an autoimmune
lymphoproliferative syndrome associated with abnormal lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99270228; PubMed-10340403; Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B., Gabr M., Roesler J.;
"Defective apoptosis due to a point mutation in the death domain CD95 associated with autroimmune lymphoma, and Hodgkin's disease.";
Exp. Hematol. 27:868-874(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,
                                                                                                                                     VARIANT ALPS TYR-260.
MEDLINE=97066823; PubMed=8929361;
Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
"Fas gene mutations in the Canale-Smith syndrome, an inherited
lymphoproliferative disorder associated with autoimmunity.";
New Engl. J. Med. 335:1643-1649(1996).
                                                                                                                                                                                                                                                                                                         Bettinaril A., Brugnoni D., Quiros-Roldan E., Malagoli A., La Grutta S., Correra A., Notarangelo L.D.; "Missense mutations in the Fas gene resulting in autoimmune lymphoproliferative syndrome: a molecular and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
MEDLINE-99126461; Pubmed-9927496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet. 64:1002-1014(1999).
                                                                                                                                                                                                                                                                          VARIANTS ALPS TRP-121 AND CYS-232. MEDLINE=97180145; PubMed=9028321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocyte apoptosis.";
J. Pediatr. 133:629-633(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunologic,
                                                                                                                                                                                                                                                                                                                                                                                     analysis.";
Blood 89:902-909(1997).
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RAY 14.00 MEDINE-21311411; PubMed-11418480; RAY 14.00 MEDINE-21311411; PubMed-11418480; RAY 14.00 MEDINE-21311411; PubMed-11418480; RAY SETAUS S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B., RAY SETAUS S.E., Jackeon C.M., Lin A.Y., Sneller M.C., Hallahan C.M., Wang J., RAY BARDAWA M.K., Grodalcky T., Fleisher T.A., Lenardo M.J.; RT The development of lymphomes in families with autoimmune in lymphocyte apoptosis."; Imphoproliferative syndrome with germline Fas mutations and defective lymphocyte apoptosis."; Blood 98:194-200(2001)
CC Tecrults caspase-8 to the activated receptor. The resulting deathing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-CC activated apoptosis may have a role in the induction of peripheral tolerance, in the antiqen-stimulated suicide of mature T-cells, or both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
CC Secreted (isoforms 2 to 6).
CC -I- SUBCELLUAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoforms 2 to 6).
CC -I- SUBCELLUAR PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d, solicing solicing and 6/TMDel/a; are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                           Groenback K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K., Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.; "Somatic Fas mutations in non-Hodgkin's lymphoma: association with extranodal disease and autoimmunity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
DISEASE Defects in TNFRSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS), also known as Canale-Smith syndrome (CSS), a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and
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                                                                                VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198; VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299. MEDLINE-99005325; Pubmed=9787134;
"The molecular basis for apoptotic defects in patients with CD95 (Fas/Apo-1) mutations.", J. Clin. Invest. 103:355-363(1999).
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SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD95 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
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EMBL; X89101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.; 
"Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation (RASL Ecceptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
LTONTKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTATSNTNCRKQSPRNRLWLLTIL
                                                                                                                                            177 VLLIPL-VFIYRKYRKRKCWKRRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIAEDM
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_1; 2.
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15-JUL-1999 (Rel. 38, Last seq
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InterPro: IPR000488; Death.
InterPro: IPR001368; TNFR_C6.
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SEQUENCE FROM N.A.
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117 LIQNIKCKCKPDFYCDSPGCEHCVRCASCEHGTLEPCTAISNINCRK-----QSPRNRLW 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWIWAVI,PLV---LAGSQLR-VHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCC 56
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                       BY SIMILARITY.
N'LINKED (GLCNAC. ..) (POTENTIAL).
N'LINKED (GLCNAC. ..) (POTENTIAL).
DEATH_DOMAIN; 1. s. Transmembrane; Glycoprotein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                             TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (PO
5B8B03682756BF1B CRC64;
                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      Score 841.5; DB 1
Pred. No. 1.2e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAECRRILDKFODMVOKDLGKSTPDTGNENEGOCL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 AA
                                                                                                                            TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
DEATH.
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MEDLINE-96226401; PubMed-8634151;
                                                                                                                                                                                                                                                                                                                                                                        37592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        46.68;
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332
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                Receptor; Apoptosis;
                                                                                                                                                                                                                                                                                                                                      38
116
332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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P51867;
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                                 SIGNAL
                                                                                                                                                            REPEAT
                                                                                                                            REPEAT
                                                                                                                                               REPEAT
                                                CHAIN
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L--LILLIPIVLIIXKVVKSRERNKKNDYCNSAASNDEGRQLNLTDVDLGKYIPSIAEQM

LIILVLLIPLVFIYRKYRKRKCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDM

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233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKK 292
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** HSSP; P25445; 1DDF.

** RIGEPPO; 1PR000488; Death.**

** InterPro; 1PR0001368; TWFR_c6.

** DR Pfam; PF00020; TWFR_c6; 3.

** DR Pfam; PF00051; DEATH; 1.

** DR SMART; SM02008; TWFR_1; 3.

** DR SMART; SM02008; TWFR_NGFR_1; 3.

** DR PROSITE; PS50050; TWFR_NGFR_2; 2.

** PROSITE; PS50017; DEATH_DOMAIN; 1.

** Anobtosis; Glycoprotein; Transmembrane; Repeat; Signal.**

** POTENTIAL.**

** POTENTIAL.*

** POTENTIAL.
inducing signaling complex (DISC) performs caspase-8 protectolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or SUBCELULAR LOCATION: Type I membrane protein.

DOWAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, SIMILARITY: CONTAINS 3 THER-CYS REPEATS.

SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 FCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVET 113
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N-LINKED (GLCNAC. . .) (POTENTIAL).
4D88A90E9E1F4892 CRC64;
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TNFR-CYS 2.
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323 AA;
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                                                                                                                                                          0902M4; 09JJL5; 09JJL6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 10B precursor (Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
"Molecular cloning and functional analysis of the mouse homologue of
the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate specific cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura'r., Tamari M., Watanabe O.;
"Mouse TRAIL receptor.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for the cytotoxic ligand TMFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney INDUCTION: TWRESTIOB is regulated by the tumor suppressor p53.
SIMILARITY: CONTAINS 3 TWER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteases) mediating apoptosis. Promotes the activation of NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homotrimer. Can interact with TRADD and RIP
                                                                                                                                             ¥.
                         293 A----LAEKICDIVMKDITNERENANLQNENENL 322
293 AECRRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
MEDLINE=99310501; PubMed=10383128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TRAIL) death receptor.";
Cancer Res. 59:2770-2775(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF176833; AAD52656.1; --
EMBL; AB031081; BAA96463.1; --
EMBL; AB031082; BAA96463.1; --
HSSP; O14763; 1D0G.
MGD; MGI:1341090; Infrsf10b.
                                                                                                                                                                                                                                                                                INFRSF10B OR DRS OR KILLER
                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                 (MK)
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                                                                                                                                           LOB_MOUSE
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HSSP; 014763; 1D0G.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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TRANSMEM
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REPEAT
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      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 PCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMD-KNHYADKCRRCTLCDEEHGLEVETNCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 LTQNTKCKCKPDFYCDSPGCEHCVRCASCEHG--TLEPCTATSNTNCRKQSP----RNR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1943 SNHNTEPGKTQKTGKKLLVPVNGNDSADDLKFIFEYCSDIVPFDSWNRLMRQLGLTDNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 QMVKAETLV-TREALYQMLLKWRHQTGRSASINHLLDALEAVEERDAMEKIEDYAVKS-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LW--LLTILVLLIPLVFIYRKYRKRK---CWKRR-QDDPES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 ------RTSSRETIPMNASNLSLS-KYIPRIAEDMT-IQEAKKFARENNIKEGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 DEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLKKAECRRTLDKFQDMVQKDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
A > V (IN REF. 1).
A -> R (IN REF. 2; BAA96463).
C -> AT (IN REF. 1).
C -> R (IN REF. 1).
C -> S (IN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 381;
                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Mismatches 122; Indels
                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                         Receptor; Apoptosis; Transmembrane; Repeat; Signal. SIGNAL 1 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272; DB 1;
Pred. No. 3.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T10A_HUMAN STANDARD; PRT; 468 AA. 000220; 096E62; 16-0CT-2001 (Rel. 40, Created) L5-UN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam: PF000531; death; 1.
SMART; SM00005; TNFR.c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOWAIN; 1.
PROSITE; PS50050; TNFR_NGFR_1; FALSE_NEG.
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TNFR-CYS 2.
TNFR-CYS 3.
DEATH.
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26.7%;
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Tumor necrosis factor receptor superfamily member 10A precursor (Death receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL receptor 1) (TRAIL-RI).
TURPESFIOA ON DR4 ON TRAIL-RI ON APO2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i. SUBGUIT: Can interact with TRADD and RIP.
-i. SUBCELLULAR LOCATION: Type I membrane protein.
-i. TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L. "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).

- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-97238921; Pubmed-9082980;
Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., N1
Dixit V.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: CONTAINS 3 THER-CYS REPEATS.
-i- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg \bar{k}_{\star, \star} Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The receptor for the cytotoxic ligand TRAIL."; Science 276:111-113(1997).
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SMART; SM00009; TURE; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TUFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_1; 2.
RECEPLOT; APOPLOSIS; Transmembrane; Gly SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98090092; Pubmed-9430227;
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InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:||| :: | | :|: | |: :| |: :| |: :| |: :| |: :| |: :|: :|: :| |: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: 
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MEDLINE-20519229; PubMed-11063728;
Engemann S., Stroedicke M.; Paulsen M., Franck O., Reinhardt R.,
Engemon S., Reik W., Walter J.;
"Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting.";
Hum. Mol. Genet. 9:2691-2706(2000).
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Q9ER63; Q8VHCO;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).
                                                                                                                                                                                                                                                                                                                                                                                        13 AGSQLRVH-----TQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQP 61
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                          .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                              Score 215; DB 1; Length 468;
Pred. No. 1.3e-09;
64; Mismatches 137; Indels 106;
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-> T (IN REF. 1).
7E9661859A550CD4 CRC64;
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                                                                                SIMILARITY.
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      TNFR-CYS 2.
TNFR-CYS 3.
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1164
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CONFLICT
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15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor
(Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 95
SEQUENCE FROM N.A.

Pan G., Mao W., Risser P.;

"Characterization of SOB, a member of the TNFR family.";

Submitted (JUL_2001) to the EMBL/GenBank/DDBJ databases.

-! SUBCELUDLAR LOCATION: Type II membrane protein (Potential).

-! TISSUE SPECIFICITY: Ubiquitous.

-! SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
EE30D617F49DBB7D CRC64;
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MGD; MGI:1930269; Tnfrsf23.
InterPro; IPR001368; TNFR_c6.
PFam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR, 3.
PROSITE; PS50050; TNFR, 3.
PROSITE; PS50050; TNFR, 3.
OYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJZ78264; CAC16405.1; -. EMBL; AAZ76505; CAC27352.1; -. EMBL; AY046550; AAL05072.1; -. HSSP; P19438; 1EXT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-CETVICAL adenocarcinoma;
MIDILINE-97053782; PubMed-8898196;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Merrees simplex virus-1 entry into cells mediated by a novel member of the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Search for polymorphisms in the genes for herpesvirus entry mediator, Nectin-1, and Nectin-2 in immune seronegative individuals."; J. Infect. Dis. 185:36-44(2002).
                                                                                                                                                                                                                                           MEDLINE-97306336; PubMed-9162061; Khom B.S., Tan K.B., N1 J., Oh K.-O., Lee Z.H., Khm K.K., Khm Y.-J., Kwon B.S., Tan K.B., N1 J., Oh K.-O., Lee Z.H., Klm K.K., Khm Y.-J., Wang S., Gentz R., Yu G.L., Harrop J., Lyn S.D., Silverman C., Porter T.G., Truneh A., Young P.R.; And Wang Y. G., Truneh A., Young P.R.; And Wang Y. G., Truneh A., Young P.R.; And Wang Y. G., Superfamily with a wide tissue distribution and involvement in lymphocyte activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
MEDDLINE-21403268; Pubmed-11511370;
Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
Elsenberg R.J., Wiley D.C.;
"Herpes simplex virus glycoprotein D bound to the human receptor
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Zhang W., Wan T., Cao X.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
MEDLINE-21629477; Pubmed-11756979;
                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 272:14272-14276(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U81232; AAD00505.1; -- EMBL, RAF153978; AAF7588.1; -- EMBL, AF373877; AAL47717.1; EMBL, AF373878; AAL47718.1; -- EMBL, BC002794; AAH02794.1; -- PDB; LJMA; 26-SEP-01. Genew; HGNC:11912; TNFRSF14.
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SEQUENCE FROM N.A.
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                                                    NCBI_TaxID-9606;
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43 NCSEGLYGGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last sequence update)
15-UNN-2002 (Rel. 14, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).
THERREY OR TXGPIL OR OX40.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                             74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT-VCEPCPPG-TYIAHLNGLSKCLQCQM 98
                                                                             Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                            · ·) (POTENTIAL).
                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                       Length 283;
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/FTId=VAR_013440.
46CE13C2C70242C1 CRC64;
                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                /FTId=VAR_013007
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TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                POTENTIAL.
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       InterPro; IFR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS60652; TNFR_MGFR_1; 1.
PROSITE; PS50050; TNFR_MGFR_2; 2.
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269 VEETIP 274
                                                                                        3D-structure.
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TRANSMEM
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                                                                                        Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive I lymbhocytes -- a molecule related to nerve growth factor receptor.", EMBO J. 9:1063-1068(1990).
-- FUNCTION: Receptor for INFSF4/OX40L/GP34.
-- SUBCELLUIAR LOCATION: Type I membrane protein.
-- ISSUE SPECIFICITY: ACTIVATED T-CELLS.
-- SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
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DTVCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNS 158
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TURF-CYS 3 (INCOMPLETE).
TURF-CYS 4.
BY SIMILARITY.
BY
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Pfam; PF00020; TNFR_c6; 3.
Prodom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR_3:
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL
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TUMOR NECROSIS FACTOR RECEPTOR
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                                                 TISSUE=T-cell;
MEDLINE=90214614; PubMed=2157591;
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Matches 64; Conserv
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                                                                                                                                                                                                                                     01-FPB-1996 (Rel. 33, Created)
01-FPB-1996 (Rel. 33, Last sequence update)
15-JON-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.".

Eur. J. Immunol. 25:926-930(1995).

-I. FUNCTION: Receptor for INFSF4/OX40L/GP34.

-I. SUBCELLULAR LOCATION: Type I membrane protein.

-I. SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
TNFR-CYS 4.
BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                             272 AA.
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                                                                                                                                                                                             PRT;
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STRAIN-BALB/c;
MEDLINE-94044750; PubMed-8228223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 151:5261-5271(1993).
176 -LVLLIPLVFIYRKYRKRKCWK 196
                                                     219 GLGLLAPLTVLLALYLLRKAWR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:104512; Infrsf4.
InterPro; IPR001368; INFR_c6.
Pfam; PF00020; INFR_c6; I.
ProDom; PD000771; INFR_c6; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z21674; CAA79772.1; -. EMBL; X85214; CAAS9476.1; -. HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                 receptor) (OX40 antigen). TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                          RESULT 11
TNR4_MOUSE
ID TNR4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
SIGNAL
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WEDLLNE-97088617; PubMed-8934525;
Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
Grinham C.J., Brown R., Farrow S.N.;
"A death-domain-containing receptor that mediates apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GHGMVSRCDHTRDT-LCHPCETG-FYNEAVNY-DTCKQCTQCNHRSGSELKQNCTPTQDT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 VCRCRPGTQPRQDSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLD 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LWIWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGFFCCQPCQP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASCE------PRNRLWLLTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q93038; Q93036; Q93037; Q92983; PY8515; Q99831; Q99722; P78507; Q93038; Q99830; Q99R86; Q14865; Q14866; Q00275; Q00276; Q00277; Q00279; Q00280; Q90ME1; Q90ME2; Q00276; Q00277; Q00278; Q00280; Q90ME1; Q90ME2; Q90ME2; Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
125-JUN-2002 (Rel. 41, Last annotation update)
136-JUN-2002 (Rel. 41, Last annotation update)
137-JUN-2002 (Rel. 41, Last annotation update)
138-JUN-2002 (Rel. 41, Last annotation update)
148-JUN-2002 (Rel. 41, Last annotation update)
157-JUN-2002 (Rel. 41, Last annotation update)
158-JUN-2002 (Rel. 41, Last annotation update)
159-JUN-2002 (Rel. 41, Last annotation update)
159-JUN-2002 (Rel. 41, Last annotation update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of death) (LARD).

THERSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
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SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Umbilical veloe endothelial cells;
TISSUE-Umbilical veloe endothelial cells;
MEDLINE-97081063; PubMed-8875942;
Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
"Signal transduction by DR3, a death domain-containing receptor related to TNFR.1 and CD95.";
Science 274:990-992(1996).
                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                          · · · ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          Length 272;
                                                                                                                                                                                                                                                                                                                                                                                 85; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GICNAC. ..) (POT)
N-LINKED (GICNAC. ..) (POT)
N-GE7BB4156F0D08E CRC64;
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                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.3e-09;
                                                                                                                                                                                                                                                                                                                          Score 202; DB 1;
                                                                                                                                                                                                                                                                                            11.2%; Sco. 26.3%; Pred. No. /... 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 AA.
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                                                                                                                                                                                                                                                           30153 MW;
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                                                                                                                                                                                                                                                                                                                                                                                     69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
      77
95
103
1123
1164
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SEQUENCE FROM N.A.
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CARBOHYD
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TRIZ_HUMAN
AC 093039,
AC 093039,
AC 093039,
DT 10-NOV-
DT 10-NOV-
DT 10-NOV-
DE TUMOT IN 10-NOV-
DE (WSL-1)
DE
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      SOLUTION
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SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE THETA-ASSOCIATED MOLECULE TRADD AND THE TURFI RECEPTOR TO THE TURFA AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain, and Fetal ling;
MEDLINE-97205335; PubMed-9052839;
MEDLINE-97205335; PubMed-9052839;
Blodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., Macdonald H.R., Tschopp J.;
"TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
Immunity 6:79-88(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLON, INTESTINE, ABUNDANTIA ELSOLARD-1A (SHOWN HERE), ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE), 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-28/LARD-2, 5/LARD-4/LARD-11, 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND 12/BETA SOLUBLE, ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOCYTES. DECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE. PTM: GLYCOSYLATED (PROBABLE).
SIMILARITY: CONTAINS 4 THRR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
                                                                                               MEDIINE-97148200; PubMed-8994832;
Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
Goddard A.D., Bauer K.D., Ashkenazi A.;
"Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-Kappa-B.";
Curr. Biol. 6:1669-1676(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappaB and induces apoptosis. May play a role in regulating lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A new death receptor 3 isoform: expression in human lymphoid cell
lines and ncn-Hodgkin's lymphomas.";
  Goodwin R.G.;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10). MEDLINE-97272273; PubMed-9114039; Screaton G.F., Xu X. N., Olsen A.L., Cowper A.E., Tan R., MCMIChael A.J., Bell J.I.; Geath domain containing receptor "LARD: a new lymphoid specific death domain containing receptor regulated by alternative pre-mRNA splicing."; Proc. Natl. Acad. SCI. U.S.A. 94:4615-4619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98113360; PubMed-9446802;
Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goc
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Bicphys. Res. Commun. 242:376-379(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 11 AND 12)
                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salles G.
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-!- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine

residue instead of arginine.

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chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dun M., Ellington A.G., Frankland J.A., Fraser A., Franch L., Garner, P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hannand S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Hukle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McChurray A.A., Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Pathlimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramasy H., Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Whitehead S.L., Whitlehead S.L., Williams L., Williams S.A., Willing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98266353; PubMed-9605317;
Singh J., Garber E., van Viljmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97189482; PubMed-9037712; Bajorath J., Aruffo A.; "Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40."; proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrari S., Giliani S., Insalaco A., Al-Ghonaium A., Soresina A.R., Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G., Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D., Plebani A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM II).
MEDLINE-21117110; PubMed-11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.
"Regulation of £ CD40 function by its isoforms generated alternative splicing.";
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3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
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PubMed=11675497;
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SCETKDLVVQQAGTNKTDVVCGPQDRLKALVVIPIIFG
RSPGSAESPGGDPHHLRDPVCHPLGAGLYQKGGQEANO
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BC8776EC2C4A5680 CRC64;
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PROSITE; PSG0052; TNFR_NGFR_1; 1.
PROSITE; PSG0050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
3D-structure; Alternative splicing; Disease mutation.
TOTAL 1.
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
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EMBL, AJ300189; CAC29424.1; --
EMBL, BC012419; AAH12419.1; --
PIR, S04460; S04460.
PDB; ICDF; 01-APR-97.
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(JUL-2001) to the EMBL/GenBank/DDBJ databases

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Schall T.C., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.; "Molecular cloning and expression of a receptor for human tumor necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91006021; PubMed-1698610; Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Aderka D., Holtwann H., Wallach D.; "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The CDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91090841; PubMed-1702293; Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K., Himmler A., Maurer-Fogy I., Kroenke M., Stratowa C., Adolf G.R., "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
                                                                                                                              01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(TUMOR necrosis factor receptor superfamily member 1A precursor (p60)
(TNF-R1) (TNF-R1) (p55) (CD120a) [COntains: Tumor necrosis factor INFRSFIA OR INFR1 OR INFR)
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Wolecular cloning and expression of the human 55 kd tumor necrosis
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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"Cloning of human tumor necrosis factor (TNF) receptor cDNA and
expression of recombinant soluble TNF-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90235284; PubMed-2158862;
Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
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                                                                              455 AA.
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MEDLINE-90235285; PubMed-2158863;
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Genomics 13:219-224(1992)
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Cell 61:351-359(1990).
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TRESULT 14
TRIA_HUMAN
TD TRIA_HUMAN
TD TRIA_HUMAN
TD 01-FEB-
DT 01-FEB-
DT 01-FEB-
DT 01-FEB-
DT 01-FEB-
DT 01-FEB-
DE (TWF-FEB-
CS NAMMEDLIN
RA GEBLIN
RA G
                                                                                                         P19438
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FISSUE-Muscle; Strausberg R.;

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TRESTILIBRIES STANDARD TO THE SEZIONE AND ADDRESS TO TRESTILIBRIES STANDARD TO STANDARD TO TRESTILIBRIES STANDARD TO TRESTILIBRIES STANDARD TO TRESTILIBRIES STANDARD TO TRESTILIBRIES STANDARD TO THE EXTRACELLULAR DOMAIN OF THRILLEADS TO HOWOTRIMERIZATION ONCE AGREGATED THE RECEPTORS DEATH DOMAINS PROVIDED A NOVEL MOLECULAR INTERRACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. THIS EXCRITIBED TO TRESTIL COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF KAAPPA B SIGNALING.

1. SUBCELLULAR LOCATION: Type I membrane protein and secreted.

2. THE DEATH DOMAIN THAT INDUCES A SAMSE IS PROBABLY IDENTICAL TO THE DOMAIN. THE DOMAIN THAT INDUCES A SAMSE IS PROBABLY IDENTICAL TO THE DOMAIN THAT INDUCES A SAMSE.

2. THE DEATH DOMAIN THAT INDUCES A SAMSE.

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5. THE DEATH DOMAIN THAT INDUCES A SAMSE.
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                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB. MEDLINE=92588809; PubMed=8387891;
Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
Broger C., Loetscher H., Lesslauer W.;
"Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteolytic processing.

DISEASE: Defects in INFRSFIA are a cause of autosomal dominant familial hibernian fever (FHF), a disease characterized by recurrent fever, abdominal pain, localized tender skin lesions and
                                                                 MEDLINE-9011021; PubMed-2153136; Engelmann H., Novick D., Wallach D.; Fngelmann H., Novick D., Wallach D.; Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."; J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
MEDLINE-97094982; PubMed-8939750;
Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
"Structures of the extracellular domain of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99213501; PubMed-10199409;
MCDETMOLT M.F., Aksentijevich I., Galon J., McDermott E.M.,
Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
Schlingen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
Hitman G.A., O'Shea J., Kastner D.L.;
"Germline mutations in the extracellular domains of the 55 kDa TNF
receptor, TYRRI, define a family of dominantly inherited
autoinflammatory syndromes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
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SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD120a entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd120a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure 4:1251-1262(1996).
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                                                    SEQUENCE OF
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TISSUE-Spleen;
MEDLINE-92039815; PubMed-1657766;
MEDLINE-92039815; PubMed-1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Tnf receptor type b.";
Immunogenetics 34:338-340(1991).
-----LTIL-----VLLIPLVFIYRKYRKRKCWK---- 196
                                                                                                      :| : | | : | | : | | 186 KKSLEC'FKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQR-WKSKLY 244
                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 1A precursor (p60)
TUNF-R1) (TWF-R1) (P55)
TWF-RSFIA OR TWFRI OR TWFR-1.
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MEDLINE-21426168, PubMed-1645445;
Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
Molecular cloning and expression of the type 1 and type 2 murine
receptors for tumor necrosis factor.";
Mol. Cell. Eiol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-91285014; Pubmed-1647956; MEDLINE-91285014; Pubmed-1647956; Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.; "Cloning, expression and cross-linking analysis of the murine p55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A. MEDLINE-9118785; PubMed-1849278; MEDLINE-91187885; PubMed-1849278; Bennett G.L., Rice G.C., Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bebo B.F., Linthicum D.S.;
"Nucleotide sequence of the TNF type I receptor from a mouse-endothelloma call line.";
Immunogenetics 39:450-451(1994).
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Eur. J. Immunol. 21:1649-1656(1991).
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                                                                            RKOSPRNRLWL-----
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P25118;
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TR1A_MOUSE
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and for commercial
                     (See http://www.isb-sib.ch/announce/
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SUPERFRANLIV MEMBER IA, MEMBRANE FORM.
TUMOR NECROSIS FACTOR BINDING PROTEIN
EXTRACELLULAR (POTENTIAL).
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Pfam; PF00020; TMFR_c6; 4.
Pfam; PF00020; TMFR_c6; 4.
Prom; Pp000771; TMFR_c6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM000208; TMFR_MGFR_1; 3.
PROSITE; PS00652; TMFR_MGFR_1; 3.
PROSITE; PS500050; TMFR_MGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal; Sign
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CYTOPLASMIC (POTENTIAL).
THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 4.
N SMASE ACTIVATION DOMAIN (NSD).
DEATH.
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  Usage by
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1 Similarity 24.7%; Pred. No. 1.2e-07;
67; Conservative 31; Mismatches 112;
modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
                                                                                                                   11, M3294; AAA03210.1;

11, M58286; AAA6753.1;

12, M63121; AAA6754.1;

13, M75864; AAA61201.1;

14, M75865; AAA61201.1;

15, M75865; AAA61201.1;

16, M75865; AAA61201.1;

17, M75865; AAA61201.1;

18, M75865; AAA61201.1;

19, M75865; AAA61201.1;

10, M75865; AAA61201.1;

11, A1522; CAA01558.1;

12, BC010140; AAH10140.1;

13, A3499; GQHUTI.

13, A35010; A35010.

13, A38208; A38208.
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InterPro; IPR001368; INFR_c6.
                                                                                                   EMBL; X55313; CAA39021.1; -.
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PDB; 1NCF; 07-DEC-95.
PDB; 1EXT; 11-JAN-97.
Genew; HGNC:11916; TNFRSF1A.
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211
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THESELLY. NECEPOLATE ALTON AND CALLE AND LANGE THE SERILLY. The adaptor molecule FRADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteclytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity).

-!-SUBUNIT: THE BINDING TO THE EXPRACELLUAR DOMAIN OF THRI LEADS TO HOWOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTS SPECIFICALLY PROTEINS SUCH AS TRASS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THERL COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).

-!-SUBLILLARITY: CONTAINS 4 THERE, VER REPEATS.
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
           Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Receptor for INFSF2/TNF-alpha and homotrimeric
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EXTRACELLULAR (POTENTIAL)
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
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M88067; AAA40465.1; JOINED.
M76655; AAA40465.1; JOINED.
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Pfam; PF00531; death; 1.
ProDom; PD000771; TNFR_c6; 1.
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InterPro; IPR001368; TNFR_C6
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SMART; SM00208; INFR;
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$19021; $19021.
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SEQUENCE FROM N.A.
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                                                                 · · · ) (POTENTIAL).
                                                       (POTENTIAL)
                                                                                                                                         10;
                                                                                                                    Length 454;
                                                                                                                  ch 10.3%; Score 185; DB 1; Length 454 I Similarity 29.2%; Pred. No. 2.7e-07; 47; Conservative 20; Mismatches 84; Indels
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-> G (IN REF. 6).
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Search completed: May 9, 2003, 17:05:45 Job time: 17.3127 secs 1/

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1804
1 MIGIWTLLPIVLTSVARLSS.......KDITSDSENSNFRNEIQSLV 335
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	20000	TOTAL TOTAL	Human cell surface	Human Fas protein.	Human Fas antigen.	hFas from plasmid	Human Fas antiqen.	Fas protein. Mamm	Amino acid encodin	CD-95 (FAS/APO-1)	Human tumour necro	Human TNFR1 protei
	1			AAR78606	AAR99681	AAR92528	AAW50289	AAW49104	AAB19341	AAB01335	AAB50517	AAW64484
	ä	; ;	13	16	17	17	18	19	21	21	22	13
	Query Match Length DR I		335	335	335	335	335	335	335	335	335	699
æ	Query		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score		1804	1804	1804	1804	1804	1804	1804	1804	1804	1804
	Result		Н	7	е	7	S	9	7	æ	6	10

Human Fas receptor Human Fas receptor Fas-delta-TM. Hom Human Fas soluble Soluble Fas recept	cance ecepto vector #1.	Secondary Control	Human Fas antigen Antigenic peptide CD44Hextra/tmFASCH/CY CD44Hextra/tmFASCY Human Fas soluble Tumour necrosis fa Rat Fas receptor.	Expression vector plasmid fragment p Plasmid fragment p Fas antigen #2. S Fas/Apo-1/CD95 Dea Fas-R protein frag Human Fas/apol pro
AAB36267 AAB50893 AAR76238 AAR99682 AAW98070	222222	AAR41688 AAR78611 AAR92530 AAB19344 AAW86241 AAY97652 AAW50288	AAW50287 AAW50037 AAY97650 AAY97651 AAR99683 ABB1155 ABB1155 AAB36228	AAR78613 AAR78612 AAR92527 AAY97654 AAW62178 AAW93611
22 22 16 17 20 21	22 12 14 17 17	114 120 120 181 181	7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	10 10 10 10 10 10
335 331 314 314 314	219 237 173 600 627 436	327 327 327 327 920 144	. 376 376 431 121 121	576 100 100 100 100 100 100 100 100 100 10
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1792 1743 1667.5 1667.5 1655.5	1225 1225 997 972 966 870.5	856 856 856 856 852 811.5	811.5 811.5 806.5 751 621.5 589 589 535.5	534.5 530 526.5 427 352
11 12 14 15 16	2210 222 223 233	3 3 2 2 2 2 2 5 4 5 4 5 4 5 6 5 6 5 6 6 6 6 6 6 6 6 6		4 4 4 4 4 0 11 13 16 4 4 4

ALIGNMENTS

T 1 084 AAR28084 standard; Protein; 335 AA. AAR28084;	12-MAR-1993 (first entry) Human cell surface antiqen.	antigen sapien	Key Location/Qualifiers Peptide 116 /label signal Protein 17335 Modified site 118120		17173 /label= /note= " 191335 /label=
RESULT 1 AAR28084 ID AAR28084 XX AC AAR28084	12-MAR- Human C	Fas ant Homo sa	Key Peptide Protein Modifie	Modifie	Domain Domain
RESULT AAR2808 ID AA XX AX	X L X B	X X X X X X X X X X X X X X X X X X X	FT FT FT FT	FT FT FT FT	FT FT FT XX

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Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                      AAR78606 (human Fas protein) is encoded by the plasmid pF58 which contains hFas cDNA. The plasmid was used in the construction of an expression vector for the proden. Of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of related diseases.
                                                                                                                                                                                                                                                                                                                                           Example 1; Pages 15-17; 51pp; Japanese.
                                                     /label= sig_peptide
17..335
/label= mat_peptide
                             Location/Qualifiers
                                                                                                                                                                       93JP-0267644
                                                                                                                                                                                                  93JP-0267644
                                                                                                                                                                                                                            (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1996 (first entry)
                                                                                                                                                                                                                                                        1995-202847/27.
                                                                                                                                                                                                                                                                                                                                                                   AAR78606 (human Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAQ95297
                                                                                                             JP07115988-A
                                                                                                                                                                      26-OCT-1993;
                                                                                                                                                                                                 26-OCT-1993;
                                                                                                                                         09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Fas antigen is implicated in apoptosis. A cDNA clone encoding the antigen was isolated (pF58) and the amino acid sequence of Fas was deduced from it. The mature protein has a calculated mol.wt. of member of the NGFR/TWFR family of cell-surface membrane proteins. The inventors claim a protein comprising at least the extracellular domain of Fas antigen.
                                                                                                                                                                                                              DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1804; DB 13; Length 335; 100.0%; Pred. No. 2.4e-151; of Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pF58; human Fas cDNa; soluble membrane protein;
antibody production; diseases; treatment; prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
                                                                                                                                               Yonehara S;
                                                                                                                 (OSAB-) OSAKA BIOSCIENCE INST
                                                                                      91JP-0125234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR78606 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                       WPI; 1992-358914/44
N-PSDB; AAQ29959.
                                                                                                                                              Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     335 AA;
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                                                        24-APR-1992;
                                                                                     26-APR-1991;
                            28-OCT-1992
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EP510691-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 335;
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR78606;
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KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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            Length 335;
                                            Indels
Query Match 100.0%; Score 1804; DB 16; Best Local Similarity 100.0%; Pred. No. 2.4e-151; Matches 335; Conservative 0; Mismatches 0;
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angioimmunoblastic lymphadenopathy; AILD.

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This sequence represents the sequence for the human Fas antigen contained within the plasmid pcEV4/hFas. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas monoclonal antibody, as well as the standard soluble Fas antigen represented by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus
                                                                                                                                                                                                                                            Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 1804; DB 17; Best Local Similarity 100.0%; Pred. No. 2.4e-151; Matches 335; Conservative 0; Mismatches 0; I
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..16
/note= "hFas signal peptide"
17..335
(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                    17.335
/note= "mature hFas"
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                                                                                                      AAR92528 standard; Protein; 335
                                                                                                                                                                                                             hFas from plasmid pCEV4/hFas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-JP00349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95JP-0025637
94JP-0154706
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISB ) JAPAN TOBACCO INC.
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N-PSDB; AAT16303.
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06-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA clone (AAT34526) codes for a membrane receptor-like protein, Fas antigen (AAR99681). It was isolated from cDNA derived from the peripheral blood monouclear cells of systemic lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy (ALLD) patients. 4 Soluble variants (AAR99682-85) were identified of the Fas antigen. These arose by alternative splicing of Fas gene transscripts. The Fas variants were present at higher levels in SLE and ALLD patients than the non-soluble Fas antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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100.0%; Pred. No. 2.4e-151;
ive 0; Mismatches 0; ]
                                                                                                 /label- Sig_peptide
17.335
/label- Mat_protein
17.173
/label- Extracellular_domain
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191.,335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 109-111; 152pp; English.
                                                                                                                                                                                                                          191..335
/label- Cytoplasmic_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou T;
                                                                 Location/Qualifiers
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Best Local Similarity 100.
Matches 335; Conservative
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                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 22-DEC-1995;
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                                                                                  Peptide
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       Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                                  The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the lst cysteine residue (preferably at least 29 residues are deleted). The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases
                                                                 181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
                                                                                                                                                                                                 301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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17..335
/label- mat_peptide
17..173
/note- "claimed fragment"
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                                                                                                                                                                                                                                                                                                                                             16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagata S, Nakamura N;
                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis modulation.
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                                                                                                                                                                                                                                                                                                                                                                        Human Fas antigen.
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                                                                                                                                                                                                                                                                                                                 AAW50289;
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RTQNTKCRCKFNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The portion of a Fas protein which can be fused to a Fc polypeptide to form a Fas-Fc fusion protein"
                                                                                                                                                                     such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                   ő
                                                                                              Length 335;
                                                                                                                                   0; Indels
                                                                                                DB 18;
                                                                                          ; Score 1804; DB 18;
; Pred. No. 2.4e-151;
0; Mismatches 0;
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100.0%;
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                                                                                          Query Match 100.
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Matches 335; Conservative
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AAB01335 standard; Protein; 335
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                                                                                                                                     The present sequence represents a Fas protein sequence used in the method of the invention. The method is concerned with reducing depletion of activated Fas expressing CD8+ T-Imphocyte killer (FR) cells in an immune cell population which also comprises of Fas-ligand (FasL)-expressing activated CD4+ cells. It involves contacting this immune cell population which would interfere with the call population protein) which would interfere with the interaction between Fas and FasL. Therefore, the method is useful for identifying suitable agents which can reduce depletion of activated Fas-expressing CD8+ TK cells in immune cell populations. Also claimed is the use of the agent in the manufacture of therapeutic compositions. Apoptosis of lymphocytes can be triggered by the interfering with this interaction, the method described and its preparations can prevent apoptosis of CD8+ TK lymphocytes caused by expression of FasL on activated CD4+ cells. Such FasL-expressing activated CD4+ cells are especially the result of CD4+ cell infection with an immunodeficiency virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). The claimed prevention of apoptosis may then allow maintenance/regeneration of cytotoxia T lymphocyte (CTL) activity the agence of the parament (prophylactic and/or therapeutic) of immunodeficiency in an agent of immunodeficiency of immunodeficiency of immunodeficiency of immunodeficiency of immunodeficiency and immunodeficiency of immunodeficiency or immunications or immunodeficiency or immunodeficiency or immunodeficiency or immunodeficiency or immunodefi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
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                                                                                                            Disclosure; Fig 7; 71pp; English.
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WPI; 1998-456867/39
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           N-PSDB; AAV32993
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Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslate region, translational start site, translational termination region or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas ligand (Fasi), or Fap-1 (Fas associated protein 1, protein tyrosine phosphatase). The antisense compounds are used to inhibit the expression of Fas, Fasi or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
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Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
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                           Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1804; DB 21; Length 335; 100.0%; Pred. No. 2.4e-151; ive 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
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                                                                                                                                                                        WO200061150-A1
                                                                                                                                                                                                                                                                                                                                                    12-APR-1999;
                                                                                                                 sapiens.
                                                                                                                                                                                                                               19-OCT-2000
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nootropic;

Human tumour necrosis factor receptor FAS protein SEQ ID NO:7. Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5;

(first entry)

15-MAR-2001

AAB50517:

TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; wasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.

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Nucleic acid encoding a TRID polypeptide, also referred to as t necrosis factor receptor 5, useful in the diagnosis, treatment prevention of cancer, autoimmune disorders and viral infection

Disclosure; Fig 2; 285pp; English.

Ruben SM, Gentz RL, Ni J;

Wei Y,

WPI; 2001-041051/05.

HUMA-) HUMAN GENOME SCI INC.

99US-0135164.

20-MAY-1999;

18-MAY-2000; 2000WO-US13515.

WO200071150-A1. Homo sapiens

10-NOV-2000

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301 ANLCTLAEKIOTIILKDITSDSENSNFRNEIOSLV 335

AAB50517 standard; Protein; 335 AA

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                    A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature Uil44 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or equilation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR 6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
                                                                                                                                                                                                                                                                                                                                              Purified or recombinant polypeptide for modulating apoptosis comprises a sequence which binds to an antibody specific for UL144 or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                     UL144; death receptor; apoptosis; programmed cell death; FAS;
INF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1804; DB 21; Length 335; 100.0%; Pred. No. 2.4e-151; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 64-65; 76pp; English.
                                                               CD-95 (FAS/APO-1) death receptor.
                                                                                                                                                                                                                    99WO-US26035,
                                                                                                                                                                                                                                            98US-0205018
                                     25-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                    WPI; 2000-423383/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                  WO200034335-A2.
                                                                                                                                           Homo sapiens.
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Matches 335;
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            AAB01335;
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                                                                                                                  human.
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The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNRP-5 or TRE)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparastic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to
                                                                                                                                                                                                                                                                                                                                                                                         parasite, bacteria and viruse, restencists and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by polypeptides are useful for treating and/or preventing diseases which bind TRID polypeptides are useful for treating and/or preventing diseases sociated with increased or decreased apoptotic cell death. The TRID polypurclectides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.
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100.0%; Pred. No. 2.4e-151;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 335; Conservative
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ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335

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DILLON P J.
DIXIT V M.
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                                                                       669 AA;
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NI J.
GENTZ
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation; agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; infection; graft rejection; antagonist; inhibitor; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a human tumour necrosis factor receptor-1 which is used in a method resulting in the isolation of a human death domain containing receptor 4, DR4. DR4 agonists are used to increase apoptosis induced by tumour necrosis factor (TNP)-family ligands, e.g. in cases of cancer, autoimmune disease, viral or other infections, inflammation, graft vs. host disease, acute or chronic graft rejection. Antagonists of BR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune deficiency syndrome, neurodegenerative disease, myelodysplastic syndrome, ischemali injury, toxin-induced liver damage, septic shock, cachexia and anorexia, also a wide range of inflammatory conditions. DR4 of fragments
                                                                                                                                                                                                                                                                                             RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding human death domain-containing receptor 4 - useful for therapeutic modulation of apoptosis, in e.g. cancer and autoimmune diseases
                                                                                                                                                                                                                    LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
               61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT
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97US-0035722.
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28-JAN-1997;
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autoimmune disorder; inflammation; cardiovascular disorder; infection;
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of the protein are used diagnostically, e.g. to detect mutant DR4 (possibly associated with disease), for isolating the DR4 related sequences and for chromosomal mapping.
                                                                                                                 Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating graft-versus-host disease, cancer, immunodeficiency
                                                                                                                                                     Indels
                                                                                                             Score 1804; DB 19;
Pred. No. 6.1e-151;
0; Mismatches 0;
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100.0%;
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                                                                                                                                 Best Local Similarity 100.
Matches 335; Conservative
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The present invention provides the protein and coding sequences for two death domain containing receptors, designated DR3 and DR3-VI. These receptors are involved in apoptosis, and the sequences given can be used in the treatment of cancers, infections, cardiovascular disorders such arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms and congenital heart defects, neurodegenerative diseases, embolisms Alzhehmer's and Parkinson's diseases, autoimmune disease such as multiple sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis, and to promote anglogenesis and wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antilnflammatory; anti-HTV; antiparkinsonian; nootropic; cardiant; vasotropic; antiallergic; antidiabetic; vulnerary; ophthalmological; antibacrerial; antidinagal; antiparasitic; gene therapy; tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder; apoptosis; cardiovascular disorder; inflammatory disease; wound; infection; neurological disease; Fas receptor; protein coordinate data.
autoimmune disease comprising administering an antibody to Death Domain Containing Receptor proteins and a second therapeutic agent -
                                                                                                                                                                                                                                                                                                                                                                            KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                                                                                                                                                                                                                                                                                                                             RIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLISNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                 1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                    immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                        Score 1792; DB 21; Length 335;
Pred. No. 2.8e-150;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50893 standard; Protein; 331
                                                                                                                                                                                                                                                        Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000; 2000WO-US14554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas receptor.
                                                                                                                                                                                                                            335 AA;
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                                                                                                                                                                                                                                                                                     Matches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2000
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                        Query Match
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isolated
                                                                                                                                                                                                                                             The present sequence is given in a specification relating to an isolated nucleic acid encoding a human tumour necrosis factor receptor TRIO. The TRIO polymorelectide, polymorphide, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of cancer, such as breast and ovarian cancer and leukaemia; autoimmune disorders such as multiple sclerosis, Crohn's disease and graft versus host disease; diseases associated with increased apoptosis such as AIDS, allowed as limb ischaemia and congenital heart defects; inflammatory such as limb ischaemia and congenital heart defects; inflammatory incovascularisation, e.g. diabetic rethinopathy; infectious diseases such as viral, fungal and parasitic infectious diseases such as wiral, bacterial, fungal and parasitic infections; and neurological diseases such as amyotrophic lateral sclerosis.
                                                                                                                                                Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders, and disorders associated with apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PCFPGERRARDCTVNGDEPDCVPCQEGREXTDKAHFSSKCRRCRLCDEGHGLEVEINCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTL/TSNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1743; DB 22;
Pred. No. 6e-146;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 ANLCTLAEKI-TIILKDITSDSENSNFRNEIQSLV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adoptive immunotherapy; transgenic anima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                  Disclosure; Fig 2; 212pp; English
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                                                (HUMA-) HUMAN GENOME SCI INC.
 99US-0142563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.6%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.6
Best Local Similarity 98.8
Matches 331; Conservative
                                                                                                                  WPI; 2001-025250/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA;
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07-JUL-1999;
15-JUL-1999;
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                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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ID AAR7

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DT 06-N

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KW Fas-
KW Gas-
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A natural, soluble Fas antigen variant (AAR99682), designated Fas dell, and other Fas variants (AAR99683-85) are derived by alternative splicing of Fas gene transcripts. A CDNA clone (AAT9527) coding for the variant was obtd. from human peripheral blood monouclear cells. The Fas dell variant lacks the transmembrane domain of insoluble Fas antigen (AAR99681). Recombinant dell variant, or fragments of it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of increased levels of soluble forms of Fas antigen can be used to diagnose autoimmune diseases, esp. systemic lupus erythematosus and angioimmunoblastic lymphadenopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                               Fas antigen: autoimmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region"
                                                                                                                                                                                                                                                                                                                                                     /note= "preferred peptide from breakpoint region (claim 4, page 132)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natural, soluble form of Fas antigen secreted by human cells is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.4%; Score 1667.5; DB 17; Length 314; 93.7%; Pred. No. 2.7e-139; 1.ve 0; Mismatches 0; Indels 21;
                                                                                                                                                                                                                                                                    are
                                                                                                                                                                                                                                                                                                                                                                                            /note= "preferred peptide from breakpoint 161..171
                                                                                                                                                                                                     /note=
17.168
/label= Extracellular_domain
/note= "the 5 C-terminal residues of the
Fas antigen extracellular domain
deleted in Fas dell"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "preferred peptide from breakpoint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
                                                                                                                                                                                  /label- Mat_protein
/note= "soluble Fas dell antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 114-16; 152pp; English.
                                                                                                                                                 /label= Sig_peptide
                                                                                                                 Location/Qualifiers
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Human Fas soluble antigen Fas dell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mountz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0371263.
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Best Local Similarity 93.7
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                  164..173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT34527.
                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLISNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA was obtd. from human lymphocytes and PCR was used to make CDNA specific for Fas-delta-TM (1.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. Insert sequence of pBluescript-Fas-delta-TM encoded the protein given in AAR76238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Pred. No. 2.7e-139;
0; Mismatches 0;
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                                                 1..16
/label= Sig_peptide
                               Location/Qualifiers
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                                                                                                                                                                                                                                                                    Shapiro JP;
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                                                                                                                                                                                                                                 (LXRB-) LXR BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.48;
                                                                                                                                                                                                93US-0152443
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Matches 314; Conservative
                                                                                                                                                                                                                                                                   Barr PJ, Kiefer MC,
                                                                                                                                                                                                                                                                                                WPI; 1995-200120/26.
N-PSDB; AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 AA;
Homo saptens
                                                                                                                                                                 15-NOV-1994;
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                                                                                              WO9513701-A
                                                                                                                               26-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                             Peptide
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AAR99682
ID AAR99
XX
AC AAR99
DX
DT 10-OC
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RIQNIKCRCKPNFFCNSTVCEHCDPCIKCEHGIIKECILISNIKCKEEGSRSNLGWLCLL 180
                                               181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                              This present sequence is a soluble Fas receptor. The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (Fasl). In some embodiments, an Fasi is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo or in vivo. Suitable immunosuppressive agents include antisense molecules that inhibit
                                                                                                                                                                                                                                                                                                                               Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psorlaais; rheumatoid arthritis; systemic lupus erythematosus; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of proinflammatory responses – using an agent which modulates FasL stimulation, used for treating graft versus host disease or autoimmune disease
                                                                                                                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                              280 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
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                                                                                                                                                                                                                                 AAW98070 standard; Protein; 314
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                                                                                                                                                                                                                                                                                                         Soluble Fas receptor.
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N-PSDB; AAX24878.
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endogenous FasL expression, soluble Fas receptors or variants, ribozymes that inhibit the endogenous expression of FasL, drugs that inhibit FasL signalling, agents that induce the endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as TGF-beta. The method can be used for treating diseases associated with an undesired FasL-mediated proinflammatory response, e.g.
                                                                                                                                                                                                                                                                                       1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH
                                                                                                                                                                                                                                                                                                           graft versus host disease, or an autoimmune disease such as systemic lupus erythematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate FasL stimulation of a proinflammatory response.
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Pred. No. 3.1e-138;
0; Mismatches 2;
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                                                                                                                                                                                                                         91.8%;
93.1%;
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Best Local Similarity 93.1
Matches 312; Conservative
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Job time: 57.6647 secs
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Matches
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Sequence 1, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 45, Appli
                                                                                ; Search time 13.1571 Seconds
(without alignments)
749.153 Million cell updates/sec
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1 MLGIWTLLPLVLTSVARLSS......KDITSDSENSNFRNEIQSLV 335
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2: /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
          GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-106-353A-7
US-09-1480-100-20
US-09-155-918-3
US-09-555-918-3
US-09-555-918-3
US-09-613-985A-3
US-09-013-895A-3
US-08-415-469-6
US-08-445A-19
US-08-445A-3
US-08-95-17083-4
US-08-95-17083-4
US-08-95-17083-4
US-08-95-445A-45
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US-08-95-445A-45
US-08-95-445A-45
US-08-95-445A-45
US-08-95-445A-45
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US-08-95-4468-45
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US-08-828-683A-22
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US-09-290-640-66
US-09-180-100-21
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                                                            OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 2, Application US/08219237B
Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: TYOH, Nacto
APPLICANT: TYOHHARA, Shin
TITE OF INVENTION: DA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE JAMES W: Hellwege
STREET: P.O. Box 2266 Eads Station
COUNTRY: USA
           Sequence Seq
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MEDIUM TYPE: Floppy disk
COMPUTER: In PC Compatible
COMPUTER: Date PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAME: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION NUMBER: US/08/219,237B
FILING DATE: 22-MR-1994
CLASSIFICATION OF ADAR OF APPLICATION NUMBER: 28,808
PURPERFENCE/DOCKET NUMBER: 516762
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100.0%; Pred. No. 1.6e-160;
tive 0; Mismatches 0;
US-09-180-100-22
US-09-180-100-9
US-09-180-100-10
US-08-2190-237B-3
US-08-477-347-14
US-08-476-86-5-5
US-08-468-560C-3
US-08-828-683A-15
PCT-US95-17083-6
US-09-042-785A-26
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
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              LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                                                   KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                   RIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                      TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                                                   APPLICANT: Daniel, Peter T.
TITLE OF INVENTION: Monoclonal Antibodies to the APO-1 Antigen
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive CITY: Lexington, MA 02173
STATE: Massachusetts
                                                                                                                                                                                                      301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                   NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERNCE/DOCKET NUMBER: CTR89-35A2
TELECOMNUNICATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAIL.
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,644
TIME DATE: 16-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/691,016 FILING DATE: 17-JUN-1991 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Krammer, Peter H.
APPLICANT: Debatin, Klaus-Michael
APPLICANT: Trauth, Bernhard C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08409338 Patent No. 5891434
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Dhein, Jens
Klas, Christiane
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Falk, Werner
Oehm Alexander
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amino acid
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US-08-409-338-1
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APPLICANT:
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                        LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                                                                                                                                                                                                                                                                           TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                         Gaps
                                                                  1 MLGIWILLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                       61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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 Score 1804; DB 2;
Pred. No. 1.6e-160;
Mismatches 0;
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100.0%; Pred. No. 1.6e-160;
ive 0; Mismatches 0;
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100.0%; Pr
tive 0;
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              Best Local Similarity 100. Matches 335; Conservative
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Best Local Similarity 100.
Matches 335; Conservative
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COGANISM: Homo sapiens
US-09-290-640-2
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US-09-290-640-2
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61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: TIOH, Nacto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VOA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1804; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-160; Matches 335; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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NAME: MURPHY JR., GERLAD M.
RECISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 703-205-8000 TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 335 amino acids TYPE: amino acid
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                                                                                                                                                                                                                       APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
ITILE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM-PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                       301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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  301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV
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                                                                                                                                                        Sequence 7, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 7:
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Best Local Similarity 100.0
Matches 335; Conservative
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; MOLECULE TYPE: protein
US-09-006-353A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
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APPLICANT: N1, Jian
APPLICANT: Rosen, Craiq A.
APPLICANT: Rosen, Janes G.
APPLICANT: Pan, Janes G.
APPLICANT: Path Janes G.
TILLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
CURRENT FILING DATE: 2000-05-05
                                                  APPLICANT: NAKAMIRA, No. 630639510

APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P

CURRENT FILING DATE: 1998-11-02

EARLIER APPLICATION NUMBER: PCT/JP97/01502

EARLIER APPLICATION NUMBER: PCT/JP97/01502

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN OFF. 2.0
                                                                                                                                                                                                                                                                                          Score 1804; DB 4;
Pred. No. 1.6e-160;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: US 60/035,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 60/132,922
           Sequence 20, Application US/09180100
Patent No. 6306395
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Patent No. 6433147
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 335; Conservative 0;
                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-180-100-20
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                                         GENERAL INFORMATION:
.09-180-100-20
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LENGTH: 335
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                                                                                                                                     Score 1804; DB 4;
Pred. No. 1.5e-160;
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ilarity 100.0%; Pred. No. 1.6e-160;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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                                                                                                                               100.0%; Scc
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09573986
Patent No. 6455040
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentID Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-05-18
                              PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Ying-Fei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Nec
FILE REFERENCE: 1488-1280004
CURRENT APPLICATION NUMBER: US
                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1488.1280004
                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-573-986-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 335; Conser
                                         SEQ ID NO 3
LENGTH: 335
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US-09-573-986-7
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SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Best Local 3
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61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L) NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: $410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LLPIPLI'VWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LLPIPLIVWYKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1804; DB 4;
Pred. No. 4.1e-160;
0; Mismatches 0;
                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202)371-2540
                                                                                                                                                                                                                                                                                                                       APPLICATICN NUMBER: US/09/013,895A FILLING DATE: 27-JAN-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-448-868-3
Sequence 3, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
APPLICANT: Ni, Jian
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                   Dixit, Vishva M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 amino acids
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                       20850
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                               181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                                                    RIQNIKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
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                                                                                                    TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1804; DB 5;
100.0%; Pred. No. 1.6e-160;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      APPLICANT:
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
                                                                                                                                                                                         301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ANICTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/17083 FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                    RESULT 9
PCT-US95-17083-2
; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09013895A Patent No. 6342363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: N1, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: CC
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US-09-013-895A-3
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Length 669; Indels 9

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RESULT 12
US-08-815-469-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 669;
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                                                                                                                                                                                                                                                                             COMPOTER: TADAY GLSK
COMPOTER: TADAY GLSK
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1804; DB 4;
100.0%; Pred. No. 4.1e-160;
tive 0; Mismatches 0;
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                                                                                                               STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: STEFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1486
TELECHMONICATION INFORMATION:
TELECHMONE: (202) 371-2600
TELEFAX: (202) 371-2540
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Ban, James G.
APPLICANT: Grit, Vishva M.
TITLE OF INVENTION: Death Dom
TITLE OF INVENTION: Superfami
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 669 annino acids TYPE: amino acid
                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 335; Conservative
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                    ZIP: 20850
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-448-868-3
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61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LLPIPLIVWVKRKEVQKTCRKHRKENGGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
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                                                          APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1488.0310003/EKS/KRM
                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fr
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                              STATE: U.S.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
"AMDITER: IBM PC COMPALIBLE
"TANDITER: TANDITER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            VEX...
VOETWARE: PATCHLL...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
Sequence 6, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1488
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
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34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Steffe, Eric K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-815-469-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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Best Local Simi
Matches 334;
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RIQNTKCRCKPWFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, WICKHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SKOUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/444,231 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
ATTORNEY AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                            301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                   298 ANLCTLAEKI-TIILKDITSDSENSNFRNEIGSLV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               ; Sequence 19, Application US/08444231
; Patent No. 565,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 314 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-444-231-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 755 Page Mi
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                Sequence 3, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR.NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.6%; Score 1743; DB 4; Length 331; 98.8%; Pred. No. 7.6e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98
CLASSIFICATION: 435
                                                                                                 301 ANICTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,936
FILING DATE: MAY-30-97
CLASSIFCATION A135
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFLATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9F379
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.8
Matches 331; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ROCKVILLE STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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US-09-086-483A-3
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241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                   61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH
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181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                               241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                   61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                        APPLICANT: SHAPINO, JOHN P.
APPLICANT: SHAPINO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
121 RIQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLLTSNTKCKEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
JRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
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Pred. No. 8e-148;
); Mismatches
                                                                                                                                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                280 ANICTLAEKIQTIILKDITSDSENSNFRNEIQSLV 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J5-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          Sequence 19, Application US/08152443A Patent No. 5663070 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             3: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 813-5600
TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.4%;
ilarity 93.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304-1018
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Best Local Similarity
Matches 314; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                            US-08-152-443A-19
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                                                                                                                                                                                                                                             RESULT 15
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May 9, 2003, 17:05:23 ; Search time 16.6994 Seconds (without alignments) 1846.092 Million cell updates/sec
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1804
1 MLGIWTLLPLVLTSVARLSS......KDITSDSENSNFRNEIQSLV 335
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	dР					
Score		Query Match Length DB	DB	ID	Description	
1804	100.0		101	US-09-826-212-7	Sequence 7, Appli	
1804	100.0		10	US-09-802-669-2		
1804	100.0		10	US-09-949-713-20	20.	
1804	100.0		10	US-09-874-138-4	Sequence 4, Appli	
1804	100.0		10	US-09-884-987-2	Sequence 2, Appli	
1804	100.0		10	US-09-935-727-9	Sequence 9, Appli	
1804	100.0		12	US-10-005-842-4	Sequence 4, Appli	
1804	100.0		6	US-10-226-296-3	, Ar	
1804	100.0		σ	US-10-226-318-3	4	
1792	99.3		6	US-09-314-889-6	Sequence 6, Appl1	
1792	99.3		10	0S-09-333-966-6		
1484	82.3	281	σ	US-09-756-854-3	Sequence 3, Appli	
1484	82.3		6	US-10-041-574-3	Sequence 3, Appli	
997	55.3		σ	us-09-925-299-960	Sequence 960, App	
997	55.3	237	10	US-09-925-299-960	Sequence 960, App	
942	52.2	167	6	US-10-112-793-22	Sequence 22, Appl	
863	49.5	157	10	US-09-949-713-15	Sequence 15, Appl	
856	47.5	327	10	US-09-802-669-66	Sequence 66, Appl	
811.5	45.0	144	10	US-09-949-713-21		

Sequence 23, Appl Sequence 22, Appl Sequence 10, Appl Sequence 11, Appl Sequence 15, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 22, Appl	Sequence 1, Appli Sequence 2, Appli Sequence 31, Appl Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
10 US-09-949-713-23 10 US-09-949-713-22 10 US-09-949-713-20 10 US-09-949-713-10 10 US-09-949-713-11 9 US-10-112-793-15 10 US-09-800-909-5 10 US-09-800-909-14 10 US-09-800-908-14 10 US-09-800-908-14 10 US-09-980-908-14 10 US-09-980-908-14 10 US-09-98-018-18 10 US-09-98-018-18 10 US-09-98-17-93-24 10 US-09-98-17-93-24 10 US-09-98-17-93-24 10 US-09-98-17-93-24 10 US-09-98-17-93-24	12 US-10-035-408-1 10 US-09-924-231-2 10 US-09-934-285-13 10 US-09-935-727-31 12 US-10-020-787-2 12 US-10-066-209-2 9 US-10-226-296-5 9 US-10-226-318-5 9 US-10-076-754-6 9 US-10-076-754-6 9 US-10-076-754-6 12 US-10-067-615-6
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ALIGNMENTS

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pplication US/098265 20010021516A1 MAYTON: ei, Ying-Fei Gentz, Reiner Kuben, Steven Ni, Jian ENTION: Tumor Necros CE: 1488 128006 CE: 1488 128006 CE: 1488 128006 CATON NUMBER: US/ NG DATE: 2001-04-05 Q ID NOS: 26 tentIn version 3.0	100.0%; Score 1804; DB 10; Length 335; Similarity 100.0%; Pred. No. 1e-130; 5; Conservative 0; Mismatches 0; Indels 0; Gaps	MIGIWTLEPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETONLEGLHHDGGFCH 60 	KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120 	RTONTKCÄCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGMLCLL 180 	LLPIPLIVWVKRKEVOKTCRKHRKENOGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240 	TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
212-7 7, App 10. US2C 11. App 11. NFORMINT: Ge 11. Ge 11. Ge 11. Ge 11. Ge 11. Ge 11. Ge 12. Ge 12. Ge 13. Ge 14. Ge 15. Ge 16.	itch al Simi 335;	MLGIWTI MLGIWTI	KPCPPGE KPCPPGE	RTONTKO 	LLPIPLI LPIPLI	TLSQVKG
RESULT 1 US-09-826-212-7 Sequence 7, A Patent NO. US GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: TITLE OF INV FILE REFEREN CURRENT APPL CURRENT APPL CURRENT FILI NUMBER OF SE SOFTWARE: PA SOFTWARE: PA SEQ ID NO 7 LENOTH: 335 TYPE: PRT CURCANISM: H ORCANISM: H	Query Match Best Local Matches 33		61	121	181	241
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Alang, Hong
APPLICANT: Alang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
PRIOR PLILNG DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
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61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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Patent No. US200200449441
GENERAL INFORMATION:
APPLICANT: NAKAWURA, No. US20020044944A110
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                               Sequence 2, Application US/09802669
Patent No. US20020004490Al
GENERAL INFORMATION:
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SEQ ID NO 2
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ORGANISM: Homo sapiens
US-09-802-669-2
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Best Local Similarity
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US-09-949-713-20
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US-09-802-669-2
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100.0%; Pred. No. 1e-130;
ive 0; Mismatches 0; Indels
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APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Tu, Guo-liang
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor 5
FILE REFERENCE: 1488.1310006
CURRENT APPLICATION NUMBER: 09/565,009
PRIOR PLING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-05-07
PRIOR PLILIATION NUMBER: 60/132,498
PRIOR FILING DATE: 1999-05-07
PRIOR PLILIATION NUMBER: 60/132,498
PRIOR PLILIATION NUMBER: 60/132,498
PRIOR PLILIATION NUMBER: 60/132,498
PRIOR PLILIATION NUMBER: 09/042,583
PRIOR PLILIATION NUMBER: 09/042,583
PRIOR FILING DATE: 1999-03-17
PRIOR PLILIATION NUMBER: 60/054,021
PRIOR FILING DATE: 1997-03-17
PRIOR PLILIATION NUMBER: 60/040,846
PRIOR PLILIATION NUMBER: 60/040,846
PRIOR PLILIATION NUMBER: 60/040,846
PRIOR PLILIATION NUMBER: 60/040,846
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PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 20
LENGTH: 335
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Patent No. US20020072091A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 335; Conservative
                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-20
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SEQ ID NO 4
LENGTH: 335
TYPE: PRT
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                                                                                                                                                                         Sequence 9, Application US/09935727

Patent No. US20020150583A1

GENERAL INFORMATION:

APPLICARIT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and FILE REFERENCE: PF454P2

CURRENT PELING DATE: 2001-08-24

PRIOR PELICATION NUMBER: 06/234, 24

PRIOR PELICATION NUMBER: 60/237, 24

PRIOR PELICATION NUMBER: 60/227, 598

PRIOR PELICATION NUMBER: 60/227, 598

PRIOR PELICATION NUMBER: 60/227, 598

PRIOR FILING DATE: 2000-01-21

PRIOR PELICATION NUMBER: 60/18, 931

PRIOR FILING DATE: 1999-12-01

PRIOR PELICATION NUMBER: 60/146, 371

PRIOR PELICATION NUMBER: 60/146, 371

PRIOR PELICATION NUMBER: 60/113, 964

PRIOR PELICATION NUMBER: 60/113, 964

PRIOR PELICATION NUMBER: 60/113, 704

PRIOR PELICATION NUMBER: 60/113, 704

PRIOR PELICATION NUMBER: 60/113, 704

PRIOR PELING DATE: 1999-04-30

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100.0%; Pred. No. 1e-130;
ive 0; Mismatches 0;
                         ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                   301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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Best Local Similarity 100.
Matches 335; Conservative
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ORGANISM: Home sapiens
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Batent No. US200201102653A1
GENERAL INFORMATION:
APPLICANT: NAGATA.
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                              Indels
                                                   Score 1804; DB lu;
Pred. No. le-130;
---hes 0;
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                                                                                                            0; Mismatches
                                                               Query Match
Best Local Similarity 100.0%;
Matches 335; Conservative 0
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US-09-884-987-2
ORGANISM: Homo sapiens
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  ; ORGANISM: Ho
US-09-874-138-4
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-09-884-987-2
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TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death Receptor 4), Member of the TNF-Receptor Superfamily and Binding to Trail (AP02-L)
                                                                 241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                      241 TLSQVRGFVRRNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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MEDION TYPE: FLORM:

MEDION TYPE: FLORY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/226,296

FILING DATE: 23-Aug-2002

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1804; DB 9;
100.0%; Pred. No. 2.3e-130;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE: CURROWN>
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
                                                                                                             301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                        Sequence 3, Application US/10226296
Publication No. US20030036168A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                                                        Gentz, Reiner L.
Dixit, Vishva M.
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Pan, James G.
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                    RESULT 8
US-10-226-296-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 335;
                                                                                                                                                             APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100 0%; Score 1804; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/042,583
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEY/Aben, A. Kenley
NAME: HOOVET, Kenley
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
                                                                                                         Sequence 4, Application US/10005842
Patent No. US20020098550Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 335 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEFAX: 3013098439
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                                                                                          US-10-005-842-4
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                                                                       RESULT 7
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CLASSIFICATION:
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US-09-314-889-6
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                                                                                                                                       241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
                  181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
                                                                                       Gaps
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/226,318
FILING DATE: 23-Aug-2002
CLASSIFICATION: CUNROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: CUNROWN>
APPLICATION NUMBER: US/09/448,868
FILING DATE: COMPROWN>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE FILIC K
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
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100.0%; Pred. No. 2.3e-130;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                           ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-318-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10226318
Publication No. US20030073187A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 669 amino acids
                                                                                                                                                                                                                                                                                                                                                      Dilication w. C. GENERAL INFORMATION:
APPLICANT: Ni, Jian
Rosen, Craig A. Pan, James G. Pan, James G.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gentz, Reiner L.
Dixit, Vishva M.
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 335; Conservative
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121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLL 180
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                                                                                                                                                                                                                                                                               9
1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGOFCH
                                                                  61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT
                                                                                        SEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.: 1100 New York Ave., NW, Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vi, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Sentz, Reiner L.
APPLICANT: Sentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1488.0310003/EKS/KRM
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FILING DATE:
FILING DATE:
FILING SAPLICATION NUMBER: 05 60/028,711
FILING DATE: 17-0CT-1996
FRIOR APPLICATION NUMBER: 05 60/013,285
APPLICATION NUMBER: 05 60/013,285
FILING DATE: 12-NAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09314889
Publication No. US20030077694A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
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ADDRESSEE: Sterne, K
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FILING DATE: 12-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                              241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                   Gaps
                                                                                                                                                    MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
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                                                                                                   Length 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 6, Application US/0933966; Patent No. US20020009773A1
; GENERAL INFORMATION:
    APPLICANT: Vu, Guo-Liang
    APPLICANT: Ni, Jian
    APPLICANT: Applicant: Dixit, Vishva
    APPLICANT: Dixit, Vishva
    APPLICANT: Dixit, Vishva
    APPLICANT: Dillon, Patrick J.
    TITLE OF INVENTION: Death Domain Containing Receptors
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C
STREET: 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US20020009773A1 Yet Assigned
                                                                                          Similarity 99.7%; Pred. No. 8.4e-130; 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...alnG DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60 / 0.
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APPLICATION NUMBER: US/08/815,469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-314-889-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: NO. U
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 17-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                      Matches 334;
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US-09-333-966-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                           Query Match
Best Local
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KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                  Length 335;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                         99.3%; Score 1792; DB 10;
99.7%; Pred. No. 8.4e-130;
1ve 0; Mismatches 1;
                                                      1488.0310003/EKS/KRM
                                                                                                                                                          LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020009773A1 Relevant
TOPOLOGY: No. US20020009773A1 Relevant
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APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome SciensTREET: 9410 Key West Avenue
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFRENCE/CDOCKET NUMBER: 1486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-756-854-3

Sequence 3, Application US/09756854

Patent No. US20020164684A1

GENERAL INFORMATION:
                                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ni, Jian
Yu, Guo-Liang
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COMPUTER READABLE FORM:
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Matches 334; Conservative
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                                                                                                                                                                                                                                      protein
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PatentIn Ver.
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SOFTWARE: Pate
SEQ ID NO 3
LENGTH: 281
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APPLICANT: Yu, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan. Ping
APPLICANT: Fan. Ping
APPLICANT: Fan. Ping
APPLICANT: Gentz, Relier L.
ITILE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT APPLICATION NUMBER: 09/527,236
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR APPLICATION NUMBER: 00/05.991
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14

PRIOR FILING DATE: 1999-05-24

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                 Length 281;
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Pred. No. 2.7e-106;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: HOOVE, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-756-854-3
               APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10041574 Patent No. US20020168359A1
                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 82.3%;
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PRIOR APPLICATION DATA:
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Best Local Similarity 83.9°
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (177)

VOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/REY: SITE
LOCATION: (187)
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                                                                                                                                                                                                                    1 MLGIWILLPLVLISVARLSSKSVNAQVIDINSKGLELRKIVITVETQNLEGLHHDGQFCH
                                                                                                                                                54;
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Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAA.02
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
                                                                                                  Length 281;
                                                                                                                                                Indels
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                                                                                                Score 1484; DB 9;
Pred. No. 2.7e-106;
0; Mismatches 0;
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                                                                                                82.3%;
83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 960
LENGTH: 237
                                                                                                Query Match 82.3
Best Local Similarity 83.9
Matches 281; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
US-10-041-574-3
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OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-960
                                                                                                                                            KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                113 RPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLXVEINCT 172
                                                                                                                                                                                                              121 RIQNIKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNIKCKEEGSRSNLGWLCLL 180
                                                                                          Gaps
                                                                      1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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0
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; Patent No. US20020055627A1
; GENERAL INPORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; TITLE REFERENCE: PAIO2
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR RELIGN NUMBER: PCT/US00/05883
; PRIOR RELIGNATION NUMBER: 60/124,270
; RIGH APPLICATION NUMBER: 60/124,270
; RIGH APPLICATION NUMBER: 60/124,270
; RIGH APPLICATION NUMBER: 05/124,270
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PATENTIN Ver. 2.0
            Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.3%; Score 997; DB 10; Length 237; Pred. No. 4.7e-69; Conservative 0; Mismatches 6; Indels
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                                              6; Indels
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     Score 997; DB 9;
Pred. No. 4.7e-69;
0; Mismatches 6;
     55.3%;
96.8%;
Query Match 55.3
Best Local Similarity 96.8
Matches 179; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 179; Conserv
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233 LLPIP 237
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US-09-925-299-960
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 1116.509 Million cell updates/sec Seconds 9, 2003, 17:02:31; Search time 28.8444 May Run on:

US-09-446-634A-22

Perfect score:

1 MLGIWTLLPLVLTSVARLSS......KDITSDSENSNFRNEIQSLV 335 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	uo	apoptosis-mediatin	FAS soluble protei	apoptosis-mediatin	len precur	1-(4,7) pr		necrosis fac	growth facto	rosis fac	B cell-associated	.gen precu	B-cell activation	necrosis fac	.gen precu		growth facto	necrosis fac	gene ox40 protein	antigen precu	rosis fac	in - vari	cal prote	protein -	delta-like homeoti	yte facto	cal prote	7	moxvm - n.	homeotic protein d
	Description	apoptosi	FAS solu	apoptosi	Fas antiqen	Fas-Delta-(4,7)	FAS solu	tumor ne	nerve gr	tumor necrosis	B cell-a	CD27 antigen	B-cell a	tumor ne	CD27 antigen	nerve gr	nerve gr	tumor ne	gene ox4	OX40 ant	tumor necrosis	G2R protein	hypothetical	gene G4R protein	delta-li	preadipocyte	hypothetical	trophozoite	T2 protein	homeotic
SUMMARIES	. QI	A40036	137383	A46484	JC2395	S58662	137384	154182	JN0006	GQHUT1	A46476	A49053	A60771	JC4302	A46517	GOHON	A26431	GOMST1	148700	S12783	A35356	D72175	T28623	D36858	S53716	A54785	T29764	C42125	GQVZML	S53718
	DB	7	~	~	~	~	~	~	-	-	~		7	7	-	-	-	-	~	7	ч	~	7	~	~	~	~	~	Н	7
	Query Match Length	335	314	327	324	149	103	435	416	455	305	250	277	461	260	427	425	454	272	271	461	349	348	349	383	385	2180	677	326	385
дÞ	Query	100.0	92.4	47.5	45.9	34.5	19.0	10.3	10.1	٠	9.6	•			8.8	٠	•	8.1	٠	٠	•	•	٠	7.7	7.6	7.3	7.3	7.2	7.2	7.2
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	Result No.	Н	7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

C-Delta-1 - chicke protein B0244.8 [1	major surface glyc T2 protein – rabbi	tumor necrosis fac	trophozoite cystei OX40 homolog - hum	gene murine tumour cysteine rich prot	thrombomodulin pre laminin beta-1 cha	hypothetical prote hypothetical prote	transcription fact laminin alpha-4 ch
150719 B88465	T30545 B43692	GORTT1 B38634	A42125 I37552	I48854 I42017	A60501 MMHUB1	T26972 T25933	138869 S68960
77 77	0 0	7	0 0	01 01	7	70	1
728 574	1014	461	1766	459	577 1786	1111	1104
7.1	6.0 6.0	6.8	6.7	6.9	9.9	6.5	6.3 6.3
128 125.5	125 124.5	122.5 121.5	121.5	120.5	119 118.5	117.5	115
30 31	33 33	34 35	36	38	40	4 4 3 3	44

ALIGNMENTS

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170	980	

apoptosis-mediating surface antigen Fas precursor - human N;Alternate names: surface antigen APO-1

C;Species: Homo sapiens (man) C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

Cyaccession: A40036; S24543; A3814, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; H. Ritch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; H. Ritch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; H. Tritle: The polypeptide encoded by the cDNA for human cell surface antigen Fas can A; Reference number: A40036; MUID:91309137; PMID:1713127
A; Status: preliminary
A; Molecule type: mRNA
A; Restances: GB:M67454; NID:9182409; PIDN:AAA63174.1; PID:9182410
B; Krammer, P. H.
S; Krammer, P. H.
A; Reference number: S24543
A; Reference number: S24543

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-335 <KRA>

A;Cross-references: EMBL:X63717; NID:928741; PID:928742 R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; J. Biol. Chem. 267, 10709-10715, 1992 A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mer A;Reference number: A38142; MUID:92268122; PMID:1375228

A;Molecule type: nucleic acid
A;Residues: 1-134,'0',136-335 <OBH>
A;Experimental source: SKW6.4 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse

A; Gene: GDB: APT1 ;Genetics:

A; Cross-references: GDB:132671; OMIM:134637

protein A,Map position: 10q24.1-10q24.1 C;Superfamily: NGF receptor repeat homology C;Keywords: apoptosis; surface antigen; transmembrane pi E;1-16/Domain: signal sequence #status predicted <SIG> F;85-128/Domain: NGF receptor repeat homology <NG4> F;85-128/Domain: transmembrane #status predicted <TMM>

Length 335; Query Match 100.0%; Score 1804; DB 2; Best Local Similarity 100.0%; Pred. No. 5e-118; Matches 335; Conservative 0; Mismatches 0; 1 MLGIWILLPLVLISVARLSSKSVNAQVIDINSKGLELRKIVITVETQNLEGLHHDGQFCH 60 1 MLGIWTLIPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQPCH 60 a à

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Gaps

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Indels

S.; Copeland, N.G.; Jen-

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R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal ass
A;Reference number: A46484; MUID:92148151; PMID:1371136
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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A; Molecule type: mRNA
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: 137383
S;Tille: Species (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are A;Reference number: 137383
A;Accession: 137383
A;Accession: 137383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Lype: mRNA
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: EMBL: 247993; NID:9728578; PIDN:CAA88031.1; PID:g695539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46484; A47254
                                                                  RIQNIKCRCKPNFFCNSTVCEHCDPCIKCEHGIIKECTLISNIKCKEEGSRSNLGWLCLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                              LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
                                                                                                                                                                                                              Score 1667.5; DB 2; Length 314;
Pred. No. 1.4e-108;
); Mismatches 0; Indels 21;
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Best Local Similarity 93.7%;
Matches 314; Conservative (
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137383
FAS soluble protein - human
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A. Accession: A46484
A. Status: preliminary
A. Mocession: A46484
A. Status: preliminary
A. Molecule 'type: minary
A. Molecule 'type: minary
A. Molecule 'type: minary
A. Molecule 'type: minary
A. Mosterimental source: BAM3 macrophage cell line
A. Mote: Sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
B. Across-references: GB: W83649; NID:9193255; PIDN:AAA37593.1; PID:9193226
A. Mote: Sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
B. Adachi, M.; Watanabe-Pukunga, R.; Naqata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A; Title: Aberrant transcription caused by the insertion of an early transposable ele
A; Reference number: A47254; MuID:93189576; PMID:7680478
A; Reference number: A47254; MuID:93189576; PIDN:AAB25700.1; PID:9298506
A; Roberimental source: MRL lpr/lpr
A; Nolecule 'type: nucleic acid
A; Roberimental source: MRL lpr/lpr
A; Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1266
C; Superimental source: MRL lpr/lpr
A; Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126850)
C; Keywords: transmembrane protein
F; 44-79/Domain: NGF receptor repeat homology <NGF>
F; 81-124/Domain: NGF receptor repeat homology <NGA>
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A; Cross-references: DDBJ:D26112; NID:9468486; PIDN:BAA05108.1; PID:d1005650; PID:9468
A; Experimental source: thymus
A; Accession: PC2246
A; Aolecule type: mRNA
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Fas antigen precursor - rat
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: JC2395; PC2246
R;Kimura, K; Wakatsuki, T; Yamamoto, M.
Bicchem: Biophys: Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in
A;Feference number: JC2395; MUID:94128114; PMID:7507668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-011-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C; Accession: 137384; 137383
B; Cascino, I.: Flucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A; Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule A; Reference number: 137383; MUID:95181785; PMID:7533181
A; Accession: 137384
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-103 <RES>
A; Residues: EMBL:Z47994; NID:9728579; PIDN:CAA88032.1; PID:9695541
A; Cosssion: 137385
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Species: Homo sapies (man)
C; Date: 24 May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C; Accession: 154182
R; Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a hncDNA library of human 12p transcribed se A; Reference number: 154182; MUID:9355381; PMID:8486360
A; Title: Construction and evaluation of a hncDNA library of human 12p transcribed se A; Reference number: 154182; MUID:9355381; PMID:8486360
A; Actus: preliminary; translated from GB/EMBL/DDBJ
A; Retaidues: 1435 < RES>
A; Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
C; Genetics:
A; Geneti
                                                      KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                    A; Cross-references: EMBL: Z47995; NID: 9728580; PIDN: CAA88033.1; PID: 9695543
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Pred. No. 4.3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                            SSRNAHSPATPSAKRKDPDLTWGGFVFFFC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.0%;
Best Local Similarity 74.5%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          FAS soluble protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-86 <RE2>
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Best Local Si
Matches 63,
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558662
Fas-Delta-(4,7) protein - human
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 01-Dec-2000
C; Accession: 558662; 557566
R; Liu, C.; Cheng, J.; Mountz, J.D.
Biochem. J. 310, 957-963, 1995
A; Title: Differential expression of human Fas mRNA species upon peripheral blood mononuc
A; Reference number: 558662; MUID:96013198; PMID:755433
A; Accession: 558662
A; Reterence number: 558662; MUID:96013198; PMID:755433
A; Reterence number: 558662; MUID:96013198; PMID:755433
A; Reterence number: 558662; MUID:96013198; PMID:755433
A; Residues: 1-149 cLIUD
R; Schatzlein, C.E.
Submitted to the EMBL Data Library, June 1995
A; Reference number: 557565
A; Reference number: 557565
A; Reterence number: 557565
A; Residues: 1-62, RPT' <KI2>
A; Cross-references: DDB:D26113; NID:9468488; PIDN:BAA05109.1; PID:d1005651; PID:9468489
A; Experimental source: liver
G; Genetics:
A; Introns: 62/1
G; Superfamily: NGF receptor repeat homology
G; Reywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <AIG>F;24-79/Domain: NGF receptor repeat homology <NGF>
F;24-79/Domain: NGF receptor repeat homology <NGF>
F;44-79/Domain: NGF receptor repeat homology <NGG>
F;11-124/Domain: NGF receptor repeat homology <NGG>
F;11-124/Domain: NGF receptor repeat homology <NGG>
F;11-148/Domain: transmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTQNTKCRCKPNFFCNSTVCEHCDPCTKCE-HGIIKECTLTSNTKCKEEGSRSNLGWLCL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILSOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 827.5; DB 2; Length 32
49.0%; Pred. No. 2.9e-50;
Live 55; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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A; Molecule type: mRNA
A; Residues: 1-132 <SCH>
A; Cross-references: EMBL:X89101; NID:g887457; PID:g887458
C; Keywords: alternative snlfding
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Pred. No. 2.7e-36;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
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78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 49.0%
Matches 164; Conservative
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QY DP	103 RCRLCDEGHGLEVEINCTRIQNTKCRCKPNFFCNSTVCE141	Oy 145PCTKCEHG- Db 153 VDPCLPCTICEENE
δλ	142HCDPCTRCEH-GIIKECTLTSNTKCKEEGSR 171	
đ	160 VGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPP 219	189
δλ	172 SNLGWLCLLLLDIPIPLIVWVKREVQKTCRKHRKENQG 208	
QQ	220 EMSGIMIMLAVLLPLAFFILLATVFSCIWKSHPSLCRKLGSLLKRRPQGEGPNPVAG 276	RESULT 9 GQHUT1
δλ	209 SHESPILNP 217	tumor necrosis factor red N;Alternate names: P55 to
qq	277 SWEPPKAHP 285	N; Contains: tumor necros C; Species: Homo sapiens
RESULT	8 L1 8	C;Date: 30-Jun-1992 #sequ C;Accession: A38208; A348 R;Fuchs, P.; Strehl, S.;
nerv N;Al	nerve growth factor receptor, low affinity precursor - chicken N;Alternate names: NGF receptor	Genomics 13, 219-224, 1 A; Title: Structure of t
C;Sp C;Da	ecies: Gallus gallus (chicken) te: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	A; Reference number: A38 A; Accession: A38208
C; Ac R; La	C:Accession: JN0006; A60504 R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid	A)Molecule Lype: DNA A;Residues: 1-455 <fuc> A:Cross-references: GR.</fuc>
A; Ti	eceptor	R; Loetscher, H.; Pan, Y Cell 61, 351-359, 1990
A; Ac A; Mo	A; Accession: JN0006 A; Molecule type: mRNA	A; Reference number: A348
A; Re	A:Residues: 1-416 <lar> A:Experimental source: embruonic object broats</lar>	A; Accession: A34899 A; Molecule type: mRNA
R; He Dev.	ler, J.G.; Fatemie-Mainie, S.; Wheeler, E.F.; Bothwell, M. Biol, 137, 287-304, 1990	A; Residues: 1-455 <loe> A; Cross-references: GB:</loe>
A; T1	A:Title: Structure and developmental expression of the chicken NGF receptor. A:Reference number: A60504. MITD: 00157140. EMTD. 0157140.	A;Experimental source: pl A;Note: part of this sequ
A; Ac	A; Accession: A60504 A; Status: prel (winerw: not commandth	R;Schall, T.J.; Lewis, Cell 61, 361-370, 1990
A; MO	Tecule type: mRNA incl compared with conceptual translation figure. 71.58 (v) 71.17 (v) 71.00 (v)	A; Title: Molecular clon A; Reference number: A34
0.00	C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of	A; Accession: A34900 A; Molecule type: mRNA
	nment: This protein is thought to form a high-affinity receptor when it associates w	A; Residues: 1-455 <sch></sch>
C; Ke	<pre>auperiaminty: nerve growth factor receptor; NGF receptor repeat homology Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t 1-20/Nomain; eignal common factor.</pre>	R; Himmler, A.; Maurer-Fog DNA Cell Biol. 9, 705-715
F;21	1-10/Commain: Signat Sequence #Status predicted <sig> 21-416/Product: Perve growth factor receptor #status predicted <mat> 21-220 Annual Command Comma</mat></sig>	A; Title: Molecular clonin A; Reference number: A3655
F; 24	24-57/Domain: GridCellular #Status predicted <ext> 24-57/Domain: NGF receptor repeat homology <ng1> 59-100/Domain: NGF receptor repeat homology <ng1></ng1></ng1></ext>	A; Accession: A36555 A; Molecule type: mRNA
F; 10. F; 14	101-139/Domain: NGF receptor repeat homology \ns2> 141-181/Domain: NGF receptor repeat homology \ns3>	A; Residues: 1-455 <him> A; Cross-references: GB:M6</him>
F; 18	189-237/Region: serine/threonine-rich 240-261/Domain: transmembrane metatich and annual 240-261/Domain: transmembrane metatich annual 240-261/Domain: transmembrane metatich annual 240-261/Domain:	A; Accession: C36555 A; Molecule type: protein
F; 26	intracellular #status predicted	

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eceptor 1 precursor [validated] - human
tumor necrosis factor receptor; TNF receptor type 1
sis factor alpha inhibitor; tumor necrosis factor binding pro
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4899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231;
    Dworzak, M.; Himmler, A.; Ambros, P.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   he human TNF receptor 1 (p60) gene (TNRF1) and localization to 208; MUID:92250049; PMID:1315717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ing and expression of the human 55 kd tumor necrosis factor r<sup>o</sup> 899; MUID:90235284; PMID:2158862
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quence, including the amino end of the mature protein, confir
M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ing and expression of a receptor for human tumor necrosis fact 300; MUID:90235285; PMID:2158863
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ogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
15, 1990
ling and expression of human and rat tumor necrosis factor rece
555; MUID:91090841; PMID:1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',16 Stein, called tumor necrosis factor binding protein, is a solu K.; Chaatry, D.; Turner, M.; Feldmann, M. M.; 7380-7384, 1990 and tumor necrosis factor (TNF) receptor CDNA and expression of 881; MUID:91017509; PMID:2170974
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nslated the codon TGG for residue 371 as Thr, AAG for residue
.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M75864; GB:M75865; GB:M75866; NID:9339748; PIDN:AAA61201.1; P.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Les:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             f tumor necrosis factor receptors (INF-Rs). The cDNA for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
--IIKECTLISNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163121; NID:9339755; PIDN:AAA36754.1; PID:9339756
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                                                                                                                                   57; MUID:91006021; PMID:1698610
                                         ::|||| ||: :|:: |
EVMVKECTATSDAECRDLHPR----
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10 LLPLVLLELLVGIYPSGVIGLVPHLGDR--EKRDSVCPQGKYIHPQN-
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A; Molecule type: protein
R; Residues: 41.43, 'X', 45-53, 'X', 55-57 <SEC>
R; Residues: 41.43, 'X', 45-53, 'X', 55-57 <SEC>
R; Gatenaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A; Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto tients:
A; Reference number: A38258; MUID:91062364; PMID:2174164
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A;Cross-references: GDB:125913; OMIM:191190
A;Cross-references: GDB:125913; OMIM:191190
A;Cross-references: GDB:125913; OMIM:191190
A;Cross-references: GDB:125913; OMIM:191190
A;Cross-references: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology (F;1-21/Domain: signal sequence factor receptor 1 #status predicted (SIG)
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted (AMI)
F;30-211/Domain: extracellular #status predicted (EXT)
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82/Domain: NGF receptor repeat homology (NGI)
F;84-126/Domain: NGF receptor repeat homology (NGI)
                                                                                                                                                                  ne
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A; Molecule : 1-13 «KEM.
R; Mosidues: 1-13 «KEM.
R; Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
Eur. J. Immunol. 20, 1167-1174, 1990
Fartitle: Tumor necrosis factor inhibitor: purlfication, NH-2-terminal amino acid sequend
A; Reference number: A60231; MUID:90292116; PMID:2113477
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A; Residues: 41-43, X', 45-53, V', 55-57, XK', 60 < CLS>
A; Residues: 41-43, X', 45-53, V', 55-57, XK', 60 < CLS>
A; Experimental source: renal failure patient urine
B; Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
J. Biol. Chem. 265, 1531-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A; Accession: A35010; MUID:90110215; PMID:2153136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.: Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
A;Reference number: A60594; MUID:89171156; PMID:2924890
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R; Kaljhara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 59, 2266-2268, 1994
A; Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A; Reference number: JC2404; MUID:95128033; PMID:7765720
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, R;Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
                                                                                                                                                            tumor
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;Residues: 41-53, X',55-144, X',146-150, X',152-186, X',188-201 <KAJ>
;Experimental source: urine
;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                       for the human p55
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                                                                                                        A;Title: Cloning and partial characterization of the promoter A;Reference number: JT0758; MUID:94085779; PMID:8262379 A;Accession: JT0758
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F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: Transmembrane #stetus predicted <NG4>
F;212-234/Domain: intracellular #stetus predicted <NG5/Domain: intracellular #stetus predicted <NG5/Domain: intracellular #stetus predicted <NG5/Domain: NGF Receptor repeat NG5/Domain: NG7-0000 NG5/Domain: NG5
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Residues: 41-45 < ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 41-60 <GAT>
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Best Local Similarity
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A; Molecule type: pro
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A; Experiment
C; Comment: T
C; Genetics:
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18;

Gaps

7 LLPLVLTS-VARLSSKSVNAQVTDINSKGLELRKTVTT----VETQNLEGLHHDGQFCHK 61

97; Conservative

4atches

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RESOURT 10

A46476

B cell-associated surface molecule CD40, long splice form - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Accession: A46476; Musculus contains an alternatively polyadenylated mRNA species of mu A; Reference number: A46476; MulD:92105763; PMID:1370315
A; Accession: A46476
A; Residues: 1-1305 crops
A; Residues: 1-13026, 1992
A; Timmunol: 149, 3921-3926, 1992
A; Timmunol: 149, 3921-3926, 1992
A; Timmunol: 149, 3921-3926, 1992
A; A; Residues: 1-287; LVV CGRIZ
C; Comment: For an alternative splice form, see PTR:A46755
C; Comment: For an alternative splice form, see PTR:A6515.
C; Comment: For an alternative splice form, see PTR:A6515.
C; Comment: For an alternative splice form, see PTR:A6515.
C; Comment: For an alternative splice form, see PTR:A6515.
C; Comment: For an alternative splice form, see PTR:A6515.
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C; Comment: For an alternative splice form see PTR:A6515.
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                                                                                                                                                                             61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120
                                                                                                                                                                                                                                                                      ----CRICDEGHGLEVEINCTRIQUIKCRCKPNFFCNST 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 VCEHCDPCTKCEHGIIKECT-----LTSNTKCKEEGSRSNL-----GWLCLL-LLPIPL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 ECVSCSNCKKS-----LECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- ETVAINLSDVDLS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG---TVHLSCQEKQNTVCTCHAGFFLREN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 TFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPIPNPLQKWEDSAHKPQSL 351
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---NSICCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 MYRYQRW-KSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSS
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                                                                                         PCPPGEFKARDCTVNGDEPDCVPCQEGKEYTDKAHF - - - - SSKCRR-
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33.1%; Pred. No. 6.8e-05;
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A; Residues: 1-461 <SUT>
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Matches 6
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A; Molecule type: mRNA
A; Residues: 1-250 cGRA>
A; Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
C; Superfaully: CD27 antigen; NGF receptor repeat homology
C; Superfaully: CD27 antigen; NGF receptor spead; NcBIP:128169)
C; Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-182/Domain: extracellular #status predicted <EXT>
F; 21-182/Domain: NGF receptor repeat homology <NG1>
F; 27-63/Domain: NGF receptor repeat homology <NG2>
E; 55-105/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                 R;Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, B.; van der Horst, G.; Ossendorp, Bur. J. Immunol. 23, 943-950, 1993
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocythe A;Reference number: A49053; MUID:93209296; PMID:8384562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
C; Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C; Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C; Accession: S04460; A60771
EMBO J. 8, 1403-1410, 1989
A; Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor A; Reference number: S04460; MUID:89356608; PMID:2475341
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A; Residues: 1-277 < STA.
A; Residues: 1-277 < STA.
A; Cross-references: EMBL: X60592; NID: 929850; PIDN: CAA43045.1; PID: 929851
B; Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 11-Sep-1998
C;Accession: A49053
                               56 GQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
AHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKC--EHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;121-179/Region: proline/serine/threonine-rich
F;183-202/Domain: transmembrane *status predicted <TMN>
F;203-250/Domain: intracellular *status predicted <INT>
F;95,162/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 GGLCCRMCEPGTFFVKDCEQDRIAAQCDPCIPGTSFSPDYHTRPHCESCRHCNSGFLIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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                                                                                                                                                                                                                                                                                                     N, Alternate names: CD27L receptor; T cell activation antigen
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A,Residues: 21-50 <BRA>
A,Experimental source: Burkitt lymphoma cell line Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 164.5; DB 1
Pred. No. 0.00024;
9; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B-cell activation protein CD40 precursor - hum. N;Alternate names: B-cell surface antigen Bp50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 EINCTRTQNTKCRCKPNFFCNSTVCEHCDP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NCTVTANAECSCSKNWQCRDQECTECDP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                                                                                                                                                                                                     mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                   153 IIKECTLTSNTKC 165
                                                                                                                                   :: | |::| |
131 VMEMATETTDTVC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                         RESULT 11
A49053
CD27 antigen precursor
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor A;Reference number: JC4302; MUID:96011645; PMID:7590278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                           59 CHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEIN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGI-IKE-CTLTSNTKCK--EEGSRSNL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 G------P-----PLIVWVK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| :::|| | :: || | | :15 SSAFEKCHPWISCETKDLVVQQAGTNKTDVVCGPQDRLRALVVIPIIFGILFAILLVLVF 214
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 IKKVAK-----KPINKAPH--PKQEPQ--EINFPD-DLPGSNTAAPVQETLHGCQPVTQE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A;Accession: PC4093
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F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54.145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              37 CCSLCQPGQKLVSDCT-EFTETECLPCGE-SEFLDTWNRETHCHQHKYCDPNLGLRVQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 RKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYIT-----TIAGVMTLSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumo F;1-29/Domain: signal sequence #status predicted <SIG> F;20-461/Product: tumor necrosis factor receptor p55 #status predicted F;34-194/Domain: extracellular cysteine rich #status predicted <EXT> F;44-82/Domain: NGF_receptor repeat homology <NGI>
                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 161; DB 2; Length 461;
Pred. No. 0.00076;
5; Mismatches 147; Indels 184;
                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                          9.0%; Score 161.5; DB 2;
26.3%; Pred. No. 0.00042;
Ive 31; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p55 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-7 <SU2>
A; Experimental source: kidney cell line 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
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                                                                                                                                                                                                                                                                                                                     26.3%;
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Best Local Similarity 18.0۰
امت 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 KGFVRKNGVNE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 DGKESRISVQE 275
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
                                                                                                                                                            Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-427 <JOH>
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C; Date: 18 Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C; Date: 18 Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C; Accession: A46517; A46454
J. Immunol. 149, 3937-3943, 1992
A; Title: Genomic organization and chromosomal localization of the human CD27 gene. A; Reference number: A46517; MUID: 93094588; PMID: 1334106
A; Reference number: A46517
A; Status: not compared with conceptual translation
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A; Modecule type: DNA
A; Residues: 1-260 <LOE>
A; Note: sequence extracted from NCBI backbone (NCBIP:120386)
A; Note: sequence extracted from NCBI backbone (NCBIP:120386)
A; Note: sequence extracted from NCBI backbone (NCBIP:120386)
A; Note: authors propose an alternative repeat pattern
B; Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
J. Immunol. 147, 3165-3169, 1991
A; Title: The T cell activation antigen CD27 is a member of the nerve growth facto
A; Reference number: A46454; MUID:92013149; PMID:1655907
A; Title: The T cell activation antigen CD27 is a member of the nerve growth facto
A; Accession: A46454
A; Molecule type: mRNA
A; Residues: 1-58, A*, 60-260 <CAM>
A; Cross-references: GB:M63928; NID:9180084; PIDN:AAA58411.1; PID:9180085
A; Cross-references: GB:M63928; NID:9186711
A; Map Position: 12p13-12p13
A; Cross-references: GDB:132582; OMIM:186711
A; Map Position: 12p13-12p13
A; Natheros: 4641; 90/1; 150/1; 180/1; 220/1
C; Superfamily: CD27 antigen; MgCreceptor repeat homology
C; Keywords: duplication; 91ycoprotein; homodimer; phosphoprotein; receptor; F; 21-20/Pomain: signal sequence #status predicted <AMTP
F; 21-20/Pomain: signal sequence #status predicted <AMTP
F; 21-30/Pomain: NGF receptor repeat homology <AMCP
F; 55-105/Domain: NGF receptor repeat homology <AMCP
F; 55-105/Domain: NGF receptor repeat homology <AMCP
F; 51-104/Domain: NGF receptor repeat homology of SAMP
F; 51-104/Domain: NGF receptor repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 GGSAHSAPAQLADADPATLYAVVDGVPP-TRWKEFVRRLGLSEHEIERLELQNGRCL 402
                                                                                                                                                                                                                             CCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCSKCRSEMSQVEISPC 117
                                                                                                                                                                                                                                                                                                                 --- RCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFC 135
                                                                                                                                                                                                                                                                                                                                                                                      118 TVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNG---TVQLPCLEKQDTICNCHSGFFL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSTVCEHCDPCTKCEHGIIKE-CTLTSNTKCKEEGSRSNLGWLCLLLLPIPLIVWV---- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RD---KECVSCVNCKNADCKNLCPATSETR----NDFQDTGTTVLL----PLVIFFGLCL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 AFFLEVGLACRYQRWKPKLYSIICGKSTPVKEGEPEPLATAPSFGPITTFSPIPSFSPTT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TFSPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPPQGAGPILPMPPASTPVPTPLPKW 343
    9
                                                    10 LLPLVL------RALLVDVYPAGVHGLVLHPG----DREKRESLCPQGKYSHPQNRSI 57
LLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH-----
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                                                                                                                                                        61 --KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFS----SKCR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KRKEVQKTCRKHRKENQGSHE---
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A46517
CD27 antigen precursor - human
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C.; Mercer, E.; Bothwell
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R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth f A;Reference number: A60204; WUID:87085574; PMID:3025363
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A; Molecule type: protein
A; Residues: 29-31, Tr', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A; Experimental squrce: melanoma cell line A875
A; Note: this sequence has been corrected by a note added in proof to follow the nucl
R; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Bjophys. 294, 244-252, 1992
A; Title: Structural domains of the extracellular domain of human nerve growth factor
A; Reference number: S21689; MUID: 92198017; PMID: 1372492
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Mol. Cell. Biol. 8, 3160-3167, 1988
A.;Tile: A constitutive promoter directs expression of the nerve growth factor recep A;Reference number: 157638; WUID:89096903; PMID:2850481
A;Recession: 157638
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-22 (RES)
A;Residues: 1-22 (RES)
A;Residues: 1-22 (RES)
A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblasto C;Comment: The cysteine-ritch region of the extracellular domain may form part or all C;Comment: This protein is thought to form a high-affinity receptor when it associate
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
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C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Reywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
C;Reywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F;1-28/Domain: signal sequence #status predicted <51G>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-55/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GQFCHKPCRPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 GKLCCOMCEPGTFLVKDCDQHRKTAQCDPCIPGVSFSPDHHTRPHCESCRHCNS--GLLV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
F;192-211/Domain: transmembrane #status predicted <TMN>F;212-266/Domain: intracellular #status predicted <INT>F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                   8.8%; Score 159.5; DB 1
llarity 34.4%; Pred. No. 0.00055;
Conservative 10; Mismatches 46
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A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
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Gaps 13;
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                                                                                                                                                                                                                                                                                           94 SMSAPCVEADDAVCRCAYGYYQDET--TGRCEAGRGL--VFSCQDKQNTVCEEC 149
                                                                                                                                                                                                                                                                                                                                         131 PN--FFCNSTVCEHCDPCTKCE--HGIIKECTLTSNTKCKEEGSRSNLGWLCLLLLPIPL 186
                                                                                                                                                                                                                                                                                                                                                                   187 IVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVMT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;251-377/Domain: intracellular #status predicted <TRM>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                            Query Match

8.8%; Score 159; DB 1; Length 427;
Best Local Similarity 25.1%; Pred. No. 0.00097;
Matches 59; Conservative 28; Mismatches 68; Indels
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Search completed: May 9, 2003, 17:07:52 Job time: 31.8444 secs

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- protein search, using sw model OM protein

; Search time 15.6873 Seconds 9, 2003, 16:58:17 Мау Run on:

(without alignments) 885.720 Million cell updates/sec

US-09-446-634A-22 Title:

1804

1 MLGIWTLIPLVLTSVARLSS......KDITSDSENSNFRNEIQSLV Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P25445 homo sapien	s ans s	P51867 bos taurus	snm s	Q63199 rattus norv	Q9qzm4 mus musculu	homod	h tum	0 homo	3 рошо	3 mus m	008727 rattus norv	homo	0 homo	2 mus m	gall	mus m	3 homo	mus m	Q9ubn6 homo sapien	~	3 h tum	2 homo	'n	P26842 homo sapien		rattu	Q8uya7 camelpox vi	Q9z0w1 mus musculu	073559 cowpox viru	_	019131 bos taurus	P25118 mus musculu
SUMMARIES	QI	TNR6_HUMAN	TNR6_PIG	TNR6_BOVIN	TNR6_MOUSE	TNR6_RAT	T10B_MOUSE	TR14_HUMAN	TR12_HUMAN	T10A_HUMAN	T10B_HUMAN	TR23_MOUSE	T11B_RAT	TNR3_HUMAN	T11B_HUMAN	T11B_MOUSE	TR16_CHICK	TR22_MOUSE	TR1A_HUMAN	TNR5_MOUSE	T10D_HUMAN	TNR7_MOUSE	T10C_HUMAN	TNR5_HUMAN	TR1A_PIG	TNR7_HUMAN	TR16_HUMAN	TR16_RAT	CRMB_CAMPS	TR16_MOUSE	CRMB_COWPX	TNR3_MOUSE	TR1A_BOVIN	TRIA_MOUSE
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095407 homo sapien	P15725 rattus norv	P20333 homo sapien	P34015 variola vir	Q28203 bos taurus	P80370 homo sapien	Q9y6q6 homo sapien	O35305 mus musculu	P29825 myxoma viru	Q09163 mus musculu	P25943 shope fibro
TR6B_HUMAN	INR4 RAT	TR1B_HUMAN	CRMB_VARV	TNR5_BOVIN	DLK_HUMAN	TR11_HUMAN	TR11_MOUSE	VT2_MYXVL	DLK_MOUSE	VT2_SFVKA
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145 8.0		•	•	•			•	•		_

ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
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MEDILINE-91309137; PubMed=1713127;
ILCh N., YON-BARG S., ISAHI A., YON-BARG N., Mizushima S.I.,
Sameshima M., Hase A., Seto Y., Nagata S.;
"The polypeptide encoded by the CDNA for human cell surface antigen
Fest can mediate apoptosis.";
Cell 66:233-243(991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
MEDLINE=95181785; PubMed=7533181;
Cascino I., Flucci G., Papoff G., Ruberti G.;
"Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";
J. Immunol. 154:2706-2713(1995).
                                       TNR6 HUMAN STANDARD; PRT; 335 AA.
P25445, Q14293; Q14295; Q14292; Q16652;
Q1-MAY-1992 (Rel. 22, Created)
O1-MAY-1992 (Rel. 22, Last sequence update)
15-JON-2002 (Rel. 41, Tast annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen."; J. Biol. Chem. 267:10709-10715(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G
"An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants
                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 5).
TISSUE-PERIPHERAL blood lymphocytes;
Schaetzlein C.E., Pochlmann R., Philippsen P., Elbel H.;
Submitted (JÜN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
MEDLINE-96238926; PubMed=8648105;
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MEDLINE=92263122; PubMed=1375228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 156:4622-4630(1996)
                                                                                                                                                                                            TNFRSF6 OR APTI OR FAS OR FASI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1). TISSUE-Urinary bladder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevents cell death in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krammer P.H.;
RESULT 1
TNR6_HUMAN
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Page

Roesler J.;

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STRUCTURE BY NMR OF 218-335.
MEDILINE-97122332; PubMed-8967952;
Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
"NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
Nature 384:638-641(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS ALPS ASP-257 AND SER-310.
MEDLINE-97180739; PubMed-9028957;
Sheller M.C., Wang J., Dale J.K.; Strober W., Middelton L.A., Choi Y.,
Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
                                                                                                                                                               VARIANT ALPS PRO-241.
MEDLINE-95300225; PubMed-7540117;
Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
Lin A.Y., Strober W. Lenardo M.J., Puck J.M.;
"Dominant interfering Fas gene mutations impair apoptosis in a human autoimmune lymphoproliferative syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT ALPS ALA-28.
MEDIJNE-97463833; PubMed-9322534;
Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J., Dale J.K., Fleisher T.A., Middelton L.A., Sneller M.C., Lenardo M.J., Straus S.E., Puck J.M.;
"Autoimmune lymphoproliferative syndrome with defective Fas: genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99038860; PubMed-9821419; Infante A.J., Britton H.A., DeNapoli T., Middelton L.A., Lenardo M. Jackson C.E., Wang.J., Fleisher T., Straus S.E., Puck J.M.; The clinical spectrum in a large kindred with autoimmune lymphoproliferative syndrome caused by a Fas mutation that impairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fas/Apol mutations and autoimmune lymphoproliferative syndrome in patient with type 2 autoimmune hepatitis.", Gastroenterology 113:1384-1389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Clincial, immunologic, and genetic features of an autoimmune
lymphoproliferative syndrome associated with abnormal lymphocyte
                                                                                                                                                                                                                                                                                                            VARIANT ALPS TYR-260.

WEDLINE-97066823: PubMed-8929361;

Drappa J., Valshnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;

Ras gene mutations in the Canale-Smith syndrome, an inherited lymphoproliferative disorder associated with autoimmunity.";

New Engl. J. Med. 338:1643-1649(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99270228; PubMed-10340403;
Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in autoimmune
immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malagoli A.,
                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bettinardi A., Brugnoni D., Quiros-Roldan E.,
La Grutta S., Correra A., Notaragelo L.D.;
"Missense mutations in the Fas gene resulting
lymphoproliferative syndrome: a molecular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                influences penetrance.";
Am. J. Hum. Genet. 64:1002-1014(1999).
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MEDLINE-97180145; Pubmed-9028321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS ALPS LYS-241 AND GLN-250.
MEDLINE-99192346; PubMed-10090885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pediatr. 133:629-633(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 89:1341-1348(1997).
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VARIANT ALPS GLY-272.
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     Strausberg R.;
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WARTANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.

WEDLINE-21311411; PubMed-11418480;
Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
Roesen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
Resen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
Resen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Marx A., Waishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
The development of lymphomas in families with autoimmune
I ymphoproliferative syndrome with germline Fas mutations and
defective lymphocyte apoptosis.";
I blood 98:194-200(5001).
LEUWCTION: Receptor for TNFFF6/FASL. The adaptor molecule FADD
recruits caspase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteolytic
cactivation which initiates the subsequent cascade of caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted isoforms 2 to 6 block apoptosis (in vitro) SUBCELLUIAR LOCATION: Type I membrane protein (isoform 1);
                      associated with autoimmune lymphoproliferative syndrome, T-cell Homatol. 27:868-874(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING CO. AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

JUBEASE: Defects in TNFRSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS), also known as Canale-Smith syndrome (CSS), a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and
                                                                                                                                                                                                                                                                                                                                     Groenback N.E., Zeuthen P.T., Ralfkiaer E., Ahrenkiel V., Andersen M. Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.; "Somatic Fas mutations in non-Hodgkin's lymphoma: association with extranodal disease and autoimmunity."; Blood 92:3018-3024(1998).
                                                                                                                                                                                                                                                                                            PHE-180; LEU-183; ILE-198;
                                                                                                                                                                          Chao M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3/Del3/e, 4/b, 5/c and 6/IMDel/a; are produced by alternative
                                                                                                                                                                                                   The molecular basis for apoptotic defects in patients with CD95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 isoforms; 1 (shown here), 2/Del2/d
                                                                                                                                                             Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H.,
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SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD95 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
                                                                                                                                GLY-260 AND ILE-270
                                                                                                                                                                                                                                                                               VARIANTS NON-HODGKIN'S LYMPHONA THR-25; PHE-180
VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
MEDLINE-99005325; Pubmed-9787134;
                    "Defective apoptosis due to a point mutation
                                                                                                                                                                                                                                            Clin. Invest. 103:355-363(1999)
                                                                                                                      VARIANTS ALPS ARG-82; PRO-250; GL; MEDLINE=99126461; PubMed=9927496;
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Z47995; CAA88033.1;
Z70520; CAA94431.1;
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                                                                                                                 Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
"Expression of apoptosis-associated genes in hibernating and stunned
woorardium of nim "
                                                                                           1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN and a secopial superfamily member 6 precursor (FASL receptor) (Apoptosis mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                               LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                      ;
0
                  Length 335;
                                                      Indels
                Score 1804; DB 1;
Pred. No. 3.9e-128;
100.0%; Scc...
100.0%; Pred. No. 3...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
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                                                      Conservative
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                                    Similarity
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                                                      Matches 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNR6_PIG
077736;
                  Query Match
                                      Best Local
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KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L--CLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYIT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 TIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTL 294
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01-0cT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Fransmembrane; Glycoprotein; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5B8B03682756BF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 332;
                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 57.1%; Score 1029.5; DB 1; al Similarity 59.1%; Pred. No. 3.8e-70; 201; Conservative 50; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
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TNFR-CYS 2.
TNFR-CYS 3.
DEATH.
                        Pfam; PF00020; TNFR_c6; 3.
Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SW00208; TNFR; 3.
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HSSP; P25445; 10DF.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C
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332 AA;
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Best Local Similarity
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P51867;
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CARBOHYD
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TRANSMEM
DOMAIN
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WEDUINE-96226401; PubMed-8634151;
WEDUINE-96226401; PubMed-8634151;
WEDUINE-96226401; PubMed-8634151;
WEDUINE-96226401; PubMed-8634151;
WEDOINE-96226401; PubMed-8634151;
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
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TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
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BY SIM
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InterPro; IPR001368; TWF_c6.
Pfam: PF00020; TWFR_c6; 3.
Pfam; PF00531; death; 1.
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SMART; SM00208; TNFR; 3.
(CD95).

TNFRSF6 OR APT1 OR FAS.

Bos taurus (Bovine).
                                                                                                  Bovidae; Bovinae; Bos.
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115
323 AA;
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Best Local Similarity
Matches 191; Conserv
                                                                                                                       NCBI_TaxID=9913
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ESTRAIN-CSTBL/63; TISSUE-Kidney;

WEDLINE-21085660; PubMed-11217851;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Radota K., Matsudi H., Gissi C., King B., Kochiwa H.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ryons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
                                                                                            RIQNIKCRCKPNFFCNSTYCEHCDPCTKCEHGIIKECTLISNTKCKEEGSRSNLGW-LCL 179
                                                                                                                                                                     LLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGV 239
                                                                                                                                                                                                                                             9
                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH
                       KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92148151; PubMed-1371136; Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S., Copeland N.G., Jenkins N.A., Nagata S.; "The cDNA structure, expression, and chromosomal assignment of the
                                                                                                                                                                                                                                                                                             240 MILSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/Sv;
Koczan D., Ibrahim S.M., Thiesen H.J.;
"Role of a mutant fas receptor in a transgenic mouse.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    300 KANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV 335
                                                                                                                                                                                                                                                                                                                                                                                          327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse Fas antigen.";
J. Immunol. 148:1274-1279(1992).
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TNR6_MOUSE
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9

Gaps

14;

Length 323; 84; Indels

Pred. No. 2.8e

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                         --- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).

--- SUBCELLULAR LOCATION: Type I membrane protein.

--- TISSUE SPECTRICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS, LIVER, LUNG, HEART, AND ADULT OVARY.

--- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynshaw-Borlis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Hayashizaki Y., Feurctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                       'Lymphoproliferation disorder in mice explained by defects in Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Apoptosis; Trānsmembrane; Glycoprotein; Repeat; Signal;
Disease mutation.
                                                                                                                                  SEQUENCE OF 1-96 FROM N.A.
MEDLINE-93189576; PubMed-7680478;
Adachi M., Watanabe-Fukunaga R., Nagata S.;
"Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr
                                                                                                                                                                                                                                                                                                                                 Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 3 THFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK002590, BAB22211.1; -. AA0295702; CAC00638.1; -1. AA7295703; CAC00638.1; JOINED. AA7295704; CAC00638.1; JOINED. S56498; AAB25700.1; JOINED. S56498; AAB25700.1; JOINED. S56486; AAB25700.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                         antigen that mediates apoptosis.";
Nature 356:314-317(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00652; TNFR NGFR_1; 2. PROSITE; PS50050; TNFR NGFR_2; 2. PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                           MEDLINE-92195401; PubMed-1372394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M83649; AAA37593.1; -.
                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95484; Infrsf6
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327
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EMBL;
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                                                                                                                                                                                                                                      mice.
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TUMOR NECROSIS FACTOR RECEPTOR

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181 LLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVM 240
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                                                                                                                                                                                                                                                                                                                                                                                                             241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK 300
                                                                                                                                                                                                                                                                                              61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCT 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                    1 MLGIWTLI.PLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL.1999 (Rel. 38, Created)
15-JUL.1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura K., Yamamoto M., Wakatsuki T.;
"A variant mRNA species encoding a truncated form of Fas antigen in
                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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                                                                                                                                                                                                                     Length 327;
                                                                                                                                                                                                                   47.5%; Score 856; DB 1; Length 32
49.4%; Pred. No. 3.6e-57;
tive 54; Mismatches 107; Indels
        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                               -> N (IN LPR).
-> R (IN REF. 3).
FGBFFC5ACE356EEE CRC64;
                          CYTOPLASMIC (POTENTIAL).
SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA.
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TNFR-CYS 2.
TNFR-CYS 3.
                 POTENTIAL.
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MEDLINE-94128114; PubMed-7507668;
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37418 MW;
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1186
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114
246
38
327 AA;
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       165;
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Q63199;
       DOMAIN
TRANSMEM
DOMAIN
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REPEAT
DOMAIN
DISULFID
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                                   REPEAT
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                U. Blochem. Biophys. Res. Commun. 198:666-674(1994).

1. FUNCTION: Receptor for TWRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-CO mediated apoptosis may have a role in the induction of peripheral both (By similarity).

1. SUBCELLIAR LOCATION: Type I membrane protein.

2. I- SUBCELLIAR COOTION: Type I membrane protein.

2. I- DOMAIN: CONTAINS TO DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, CONTAINS TO THE CYS REPEATS.

2. I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMAKI; SMUGACO, 4...., PREMICE 1; 2. PROSITE; PSG0652; TNFR_MGFR_1; 2. PROSITE; PSS00650; TNFR_MGFR_2; 2. PROSITE; PSS0017; DEATH_DOMAIN; 1. Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal. SIGNAL BY SIMILARITY BY SEMILARITY PROFESSION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RIQNIKCRCKPNFFCNSTVCEHCDPCTKCE-HGIIKECTLTSNTKCKEEGSRSNLGWLCL
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TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
THR-CYS 1.
THER-CYS 2.
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BY SIMILA
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InterPro: IPR001368; TNFR_c6.
Pfam: PF00020; TNFR_c6; 3.
Pfam: PF00531; death; 1.
SMART: SM00005; DEATH; 1.
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HSSP; P25445; 1DDF.
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324 AA;
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       the rat
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Best Local
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                                                                                                                                                                                                                                                                                                                 Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).
TUFRSF10B OR DIS OR KILLER.
MIS miseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.; "Molecular cloning and functional analysis of the mouse homologue of the KILLER/DRS tumor necrosis factor-related apoptosis-inducing ligand
LLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGV
                                                          240 MTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLK
                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney
--- INDICTION: TWERSETOB is regulated by the tumor suppressor p53.
--- SIMILARITY: CONTAINS 3 TWER-CYS REPEATS.
--- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
                                                                                                                                                        KANLCTLAEKIQTIILKDITSDSENSNFRNEIQSL 334
                                                                                                                                                                         381 AA.
                                                                                                                                                                                                                                                                    0902M4; 09JJI5; 09JJL6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
MEDLINE=99310501; PubMed=10383128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TRAIL) death receptor.";
Cancer Res. 59:2770-2775(1999).
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF176833; AAD52656.1; -
EMBL; AB031081; BAA96462.1; -
EMBL; AB031082; BAA96463.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 014763; 1D0G.
MGI:1341090; Infrsf10b.
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U70321; AAB58354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:11912; TNFRSF14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HveA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
  10;
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092956; Q9UM65; Q96J31; Q8WXR1;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2002 (Rel. 41, Last annotation update)
15-UON-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor
(Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHG--IIKECTLTSNTKCKEE---GSRSNLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LWIGLLVPVVLLIGALLVWKTGAWRQWLLCIKRGCERDPESANSVHLSLLDRQTSSTTND 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 HRKENQGSHESPTLNPETVAINLSDV--DLSKYITTIAGVMTLSQVKGFVRKNGVNEAKI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 SNHNTEPGKTQKTGKKLLVPVNGNDSADDLKFIFEYCSDIVPFDSWNRLMRQLGLTDNQI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKA-HFSSKCRRCRLCDEGHGLEVEINCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ITTINTVCRCKPGTFEDKDSPEICQSCSNCTDGEEELTSCTPRENRKCVSKTAWASWHKLG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KEVQKTCRK 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
TURR-CYS 1.
TURR-CYS 2.
TURR-CYS 3.
TURR-CYS 3.
TURR-CYS 3.
DEATH.
BY SIMILARITY.
CHOOLING STANDARD STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 211.5; DB 1; Length 381;
Pred. No. 7.7e-09;
Mismatches 133; Indels 53;
                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                              SUPERFAMILY MEMBER 10B.
                                                                                                                                                                                                                              Receptor; Apoptosis; Transmembrane; Repeat; Signal.
SIGNAL 1 52 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 WICLILIPI ----PLIVW-----VKR-----
                                                                                             SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00052; TNFR_NGFR_1; FALSE_NEG.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 24.2%;
                                             Pfam; PF00531; death; 1. Pfam; PF00020; INFR_c6; 2.
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381 AA;
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                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
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DOMAIN
DISULFID
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REPEAT
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1D TR14_H
C 092956
DT 16-02T
DT 16-0CT
DT 15-JUN
DE TUMOR
DE (HEYPO
C HRYPE
C TNPRSF
                                                                                                                                                                                                                                                                                   CHAIN
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Matches
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DORAN 
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-1- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
TNFSF1/1/mphotoxin-alpha. Involved in lymphocyte activation. Plays
an important role in HSV pathogenesis because it enhanced the
entry of several wildtype HSV strains of both serotypes into CHO
cells, and mediated HSV entry into activated human T cells.
-1- SIBCELLUIAR LOCATION: Type I membrane protein (Probable).
-1- TISSUE SPECIFICITY: WIDELX EXPRESSED, WITH THE HIGHEST EXPRESSION
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Cervical adenocarcinoma;
TISSUE-Cervical adenocarcinoma;
MEDILINE-97053782; PubMed-8898196;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
Therpes simplex virus-1 entry into cells mediated by a novel member of the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pear P.G.; Search for polymorphisms in the genes for herpesvirus entry mediator, sectin-1, and Nectin-2 in immune seronegative individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J., Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C., Porter T.G., Truneh A., Young P.R.; an awaly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
MEDLINE-2140326B; PubMed-11511370;
MATILLS-3140326B; PubMed-11511370;
MATILIS S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
Eisenberg R.J., Wiley D.C.;
sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
olta: Rutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Herpes simplex virus glycoprotein D bound to the human receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
MEDLINE-21629477; PubMed-11756979;
Struyf F., Posavad C.M., Reyaerts E., Van Ranst M., Corey L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. 2. 2 ao X.; 2. 2 august Wan T., Cao X.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte activation.";
J. Biol. Chem. 272:14272-14276(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , U70321; AAB5835...;
, U81232; AAD00505.1;
, AF153978; AAF75588.1; -...
, 7733877; AAL47777.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-97306336; Pubmed-9162061;
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J. Infect. Dis. 185:36-44(2002).
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NCBI_TaxID=9606;
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                   NAMES OF STREET 
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                                                                                                                                                                                                                    Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D TRI2_HUMAN STANDARD; PRT; 417 AA. (99912; P78507; Q99038; Q93038; Q93038; Q93038; Q93038; P78515; Q99831; Q99722; P78507; Q99830; Q998806; Q99W865; Q14865; Q14865; Q00275; Q00277; Q00278; Q00279; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
K -> R.
                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.4%; Score 206; DB 1; Length 28 25.0%; Pred. No. 1.4e-08; Live 30; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_013440.
46CE13C2C70242C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
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/FIId=VAR_013007.
V -> T
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TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 1. PROSITE; PS50050; TNFR_NGFR_2; 2.
                   TINCETPIC) IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
Probom; PD000771; TNFR_C6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 AA; 30392 MW;
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                                                                                                                     SMART; SM00208; TNFR; 3
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TISSUE-Lymphoid;
MEDLINE-97088617; PubMed-8934525;
Kitson J., Ravon T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
Grinham C.J., Brown R., Farrow S.N.;
"A death-domain-containing receptor that mediates apoptosis.";
Nature 384:372-375(1996).
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MEDLINE-97205335; PubMed-9052839;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., Macdonald H.R., Tschopp J.;
"TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNRF1 RECEPTOR TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Ashkenazi A.;

"Apo-3, a new member of the tumor necrosis factor receptor family, contrains a death domain and activates apoptosis and NF-kappa-B.";

Curr. Biol. 6:1669-1676(1996).
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"A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas.";
Biochem. Biophys. Res. Commun. 242:376-379(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodwin R.G.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Umbilical vein endothelial cells;
MEDLINE-97081063; PubMed-8875942;
Chinnanyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
Signal transduction by DR3, a death domain-containing receptor related to TNRR-1 and CD95.";
Science 274:990-992(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10). MEDLINE=97272273; PubMed=9114039; Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.I.; Isoformatic a new lymphole-specific death domain containing receptor regulated by alternative pre-mRNA splicing."; Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
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SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
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Shlozawa S., Konlshi Y., Murayama K., Mukae N., Yamamoto Shlozawa S., Satto M., Shlozawa K., Tsukamoto Y.; Satto M., Shlozawa K., Tsukamoto Y.; Submitted (NoV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goo
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch.ch).
                                                                       ALTERNATUT.

AND SPECIFICITY:

AND SPLEEN.

 ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
               NF-KAPPA B SIGNALING. SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
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Pfam; PF00020; TNFR.C5, 2.
Pfam; PF00531; death; 1.
PROSITE; PS00052; TNFR.NGFR.1; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal; Repeat; Polymorphism.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
THRF-CYS 1.
THRR-CYS 3.
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U83600; AAB41935.1;
U78029; AAB40918.1;
U74611; AAB39714.1;
U94501; AAC51309.1;
U94504; AAC51309.1;
U94505; AAC51310.1;
U94505; AAC51311.1;
U94509; AAC51311.1;
U94509; AAC51313.1;
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U94510; AAC51313.1;
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InterPro; IPR001368; TNFR_c6.
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TYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLA
PPDSSERICTVQLV -> PPPSLAGAFWGAVQSAVPLSVAG
PPDSSERICTVQLV -> PPPSLAGAFWGAVQSAVPLSVAG
RYGGVLGARVGELGWTEGRRVRRGATTQHPPAAFSVLGPG
APGWPCGPPPAWGHPDLHIPPLLASQAPGYCR (IN
ISOFORM 12)
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MISSING (IN ISOFORM 5).
STLGSCPERCAAVCGWRQM -> PPPSLAGAPWGAVGSAVP
LSYAGGRVGV (IN ISOFORM 11).
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MFWYQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
MEALTPPPATHLS -> SRWCAGNARGRIGMDRGEAGEEGG
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                                                                                                                                                                                                                                                                                                            MISSING (ÎN ISOFORM 8).
SRRDTDCGTCLPGFYE -> HPSVTLGQRPHPSSTS (IN
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6, ISOFORM 7 AND
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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 INFR-CYS 4.
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000220; Q96E62;
16-OCT-2001 (Rel. 40, Created)
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21.48;
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Euteleostomi;

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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 10A precursor (Death receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL-R1)
THERSF10A OR DR4 OR TRAILR1 OR APO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1. SUBGUIT: Can interact with TRADD and RIP.
-1. SUBGUIT: Can interact with TRADD and RIP.
-1. SUBCELLUIAR LOCATION: Type I membrane protein.
-1. TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.
-1. SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
-1. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98090092; PubMed-9430227;
Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.
"Death receptor 5, a new member of the TNFR family, and DR4 induce
Imbordependent apoptosis and activate the NF-kappaB pathway.";
-I. FUDD-dependent apoptosis and activate the NF-kappaB pathway.";
-I. FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
adaptor molecule FADD recruits caspase-8 to the activated
receptor. The resulting death-inducing signaling complex (DISC)
performs caspase-8 porteolytic activation which initiates the
subsequent cascade of caspases (aspartate-specific cysteine
proteases) mediating apoptosis. Promotes the activation of NF-
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                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-97238921; Pubmed-9082980;
MEDLINE-97238921; Chinnaiyan A.M., Gentz R., Ebner
Dixit V.M.,
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The receptor for the cytotoxic ligand TRAIL."; Science 276:111-113(1997).
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InterPro; IPR001368; TWFR_C6.
Pfam: PF00050; TWFR_C6; 2.
Pfam: PF00531; death; 1.
SWART; SW0005; DEATH; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS00052; TWFR_NGFR_1; 2.
PROSITE; PS00505; TWFR_NGFR_1; 2.
PROSITE; PS00505; TWFR_NGFR_1; 2.
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HSSP; 014763; 1D0G.
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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240
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SIGNAL
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TISSUB-Foreskin fibroblast;
MEDLINE-97459925; PubMed-9311998;
Walczak H., Degil.-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,
Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,
Goodwin R.G., Rauch C.T.;
                                                                                                                                                                                                                                                                62 P----CPPGERKARDCTVNGDEPD-CVPCQEGKEYTDKAHFSSKCRRCRLC--DEGHGLE 114
                                                                                                                                                                                                                                                                             115 VEINCTRIQNTKCRCKPNFFCNSTVCEHCDPCTK-CEHGI--IKECTLTSNTKC--KEEG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                           251
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                                                                                                                                                                                                                                                                                                                                                                                                                                              356 NGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTAGPGDALYAMLMKW 415
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                                                                                                                                    .) (POTENTIAL).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                     HESPTLNPETVAINLSDVDL-SKYITTIAGVMTLS------QVKGFVRK----
                                                                                                                                                                                     DB 1; Length 468;
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-> T (IN REF. 1).
7E9661859A550CD4 CRC64;
   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                       62; Mismatches 126;
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Pred. No. 1.1e-07;
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           TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                         DEATH.
POLY-ALA.
                                                                                                                                                               50061 MW;
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21.1%;
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1145
1188
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468 AA;
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Goddard A.D., Godowski P., Ashkenazi A.; "Control of TRAIL-induced apoptosis by a family of signaling and decoy
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Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
"Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Ovary;
MEDLINE-97467719; PubMed-9326928;
Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,
Wu G.S., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.,
"KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G., Ni J., Wel Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
antagonist decoy receptor and a death domain-containing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood I Dackt receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).
                                                                                                        Screaton G.R., Mongkolsappya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.; Trickl, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL."; Curr. Blol. 7:693-696(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97390509; PubMed-9242611;
Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
                                                      SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE
"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
EMBO J. 16:5386-5397(1997).
                                                                                                                                                                                                                                                                               Holler N.,
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                        (LONG ISOFORM), AND CHARACTERIZATION
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SEQUENCE FROM N.A. (SHORT ISOFORM).
Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;
                                                                                                                                                                                                                                                                             Schneider P., Bodmer J.-L., Thome M., Hofmann K.,
                                                                                                                                                                                                                                                                                                                 "Characterization of two receptors for TRAIL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blol. Chem. 272:25417-25420(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (SHORT ISOFORM). MEDLINE-97467318; Pubmed-9325248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (SHORT ISOFORM). MEDLINE-97390508; Pubmed-9242610;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG ISOFORM)
TISSUE-Liver, and Spleen;
MEDLINE-98039016; PubMed-9373179;
                                                                                         MEDLINE-97431692; PubMed-9285725;
                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 416:329-334(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Genet. 17:141-143(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 277:818-821(1997).
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                                                                                                                                                                                                                                                                                                  Ischopp J.;
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TABPEAL TO SUBCELLULAR LOCATION: Type I membrane protein.

-1 SUBCELLULAR LOCATION: Type I membrane protein.
-1 SUBCELLULAR LOCATION: Type I membrane protein.
-1 SUBCELLULAR LOCATION: Type I membrane protein.
-1 SUBCELLULAR LOCATION: Type I membrane protein.
-1 AND A SHORT FORM/TRICK2A; A REE PRODUCED BY ALTERNATIVE SPLICING.
-1 TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues; covery highly expressed in tumor cell lines such as Hele 33, K562, HL-60, SW480, A549 and G361; highly expressed in heart, peripheral blood lymphocytes, liver, pancreas, spleen, thymus, prostate, covary, uterus, placenta, testis, esophagus, stomach and throughout the intestinal tract; not detectable in brain.
-1 INDUCTION: TWERSF10B is regulated by the tumor suppressor p53.
-1 INDUCTION: TWERSF10B is regulated by the tumor suppressor p53.
-1 INDUCTION: TWERSF10B may be a cause of squamous cell carcinoma of the head and neck.
-1 SIMILARITY: CONTAINS 3 TWERCYS REPEATS.
-1 SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                         Pubmed 1034 cycyo; Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R.; Screaton G.R.; Structure of the TRAIL-DRS complex reveals mechanisms conferring specificity in apoptotic initiation."; Mat. Struct. Biol. 6:1048-1053(1999).

-! FUNCTION: Receptor for the cytocoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolylic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-
                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
MEDLINE-200107054, PubMed-10549288;
Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;
Triggering cell death: the crystal structure of ApolL/TRAIL in a complex with death receptor 5.";
Mol. cell 4:563-571(1999).
"Homo sapiens homolog of tumor necrosis factor receptor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                             Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
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                                                       SEQUENCE FROM N.A. (LONG ISOFORM)
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AAC01565.1;
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AF153687;
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                      REAL TO THE STATE OF THE STATE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | ||: |: | ||: |
84 GHH-----ISEDGRDCISCKYGQDYSTHWNDLLFCIRCTRCDSG---EVELSPCTTTRN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 TKCRCKPNFFCNSTYCEHCDPC-TKCEHGIIK--ECTLTSNTKC--KEEGSRSNLGWLCL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 TVCQCEEGTFREEDSPEMCRKCRIGCPRGMVKVGDCTPWSDIECVHKESGT----- 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 LVLVVAAVLLL----VSAESALITQQDLAPQQRAAPQQKRSSPSEGL------CPP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09ER63; 08VHC0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
factor receptor p60 homolog 1) (TNF receptor family member SOB).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 197; DB 1; Length 440;
Pred. No. 1.1e-07;
34; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 GVM------NDNV 267
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TUFR-CYS 1.
TUFR-CYS 2.
TUFR-CYS 3.
                                                                                                                                                                                                                                                                                                   PROSITE; PSS0017; DEATH DOMAIN; 1.
PROSITE; PSS0017; DEATH DOMAIN; 1.
PROSITE; PSS0050; TUFR_NGFR_1; 2.
PROSITE; PSS50050; TUFR_NGFR_2; 2.
Acceptor; Apoptosis; Transmembrane; Repeat; Signal; Signal, Signal
Signal
Signal
55
CHAIN
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440
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POLY-GLY.
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                                                                                                                    PDB; 1D0G; 22-0CT-99.
PDB; 1D4V; 01-NOV-99.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6; Pfam; PF00520; TNFR_C6; 2.
FMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
     AF192548; AAF07175.1; -. BC001281; AAH01281.1; -.
                                                  HGNC:11905; TNFRSF10B.
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26.6%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is a long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
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                                           Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.; "Sequence and functional comparison in the Beckwith-Wiedemann region: Implications for a novel imprinting centre and extended imprinting."; Hum. Mol. Genet. 9:2691-2706(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.

DOMAIN

10 9 CYTOPLASMIC (POTENTIAL).

TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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                                                                                                                                                   LINKED (GLCNAC. . .) (POTENTIAL)
EE30D617F49DDB7D CRC64;
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STRAIN-129/Sv; TISSUE-Embryonic stem cells;
MEDLINE-20519229; PubMed-11063728;
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TNFR-CYS 2.
TNFR-CYS 3.
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EMBL; AJ276505; CAC27352.1; -
EMBL; AX046550; AALO5072.1; -
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MGD; MG1:1930269; Tnfrsf23.
InterPro; IPR001368; TNFR_c6.
Ffam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
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                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                            Matches
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DEATH 2.
INVOLVED IN DIMERIZATION (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;

"Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; Glycoprotein; Repeat; Signal.
1 21 BY SIMILARITY.
                                    401 AA.
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PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                             TISSUE-Embryonic intestine;
MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000188; Death.
InterPro; IPR001368; INFR_c6.
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ProDom; PD000771; TNFR_c6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U94330; AAB53707.1; -.
HSSP; P25942; 1CDF.
                                    STANDARD;
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269
365
100
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62
80
                                                                                                                                                (Osteoprotegerin).
INFRSF11B OR OPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of bone density.";
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thomor necrosis factor receptor superfamily member 3 precursor (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor)
EVER OR THERST OR THECR.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSSKCRRCR-LCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVC---EHCDP----- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TCRKHRKENQGSHESPTLNPE----TVAINLSDVDLSKYITTIAGVMTLSQV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CIRCEHGIIKECILISNIKCKEEGSRSNLGWLCLLLLLPIPLIVWVKRKEVQK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNATHDNVCSGNREATONCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTK---- 231
                                                                                                                                                                                                                                                                                              Match 10.3%; Score 186; DB 1; Length 401; Local Similarity 25.8%; Pred. No. 6.6e-07; los 77; Conservative 36; Mismatches 110; Indels 76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                TIVETQNIEGLHHDGQ-----FCHKPCPPGERKARDCIVNGDEPDCVPCQEGKEYIDKAH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 KGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLC 304
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N-LINKED (GLCNAC. ..) (POTEWIIAL).

WHY FECGA31F1D4E573A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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MEDLINE-93252381; PubMed-8486360;
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       83
87
124
145
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165
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401 AA;
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         MEDLINE-99223511; PubMed-10207006; Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.; "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
                                                                                    Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR SUPERPAMILY MEMBER 3. EXTRACELLULAR (POTENTIAL).
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1larity 25.3%; Pred. No. 7.9e-07;
Conservative 25; Mismatches 8;
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                                                Biol. Chem. 274:11868-11873(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILAN
                                                                             MEDLINE=20261554; PubMed=10799510;
                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
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P25942; 1CDF.
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81
124
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211
                                       death in HeLa cells.
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82
125
169
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Simonet W.S., Lacep D.L., Dunstan C.R., Kelley M., Chang M.-S., Lacep D.L., Dunstan C.R., Relley M., Chang M.-S., Lacep D.L., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Campbell P., Sander S., Van G., Tarpley J., Hill D., Pattison W., Suggs S., Boyle W.J., Van G., Tarpley J., Derby P., Lee R., "Osteoprotegerin: a novel secreted protein involved in the regulation
                                100 LCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDE 159
                                                                               -TKCEH-GIIKEC--TLTSNTKCK---EEGSR 171
                                                                                                SNLGWLCLLLLPIPL------IVWVKRKEVQKTCR-----KHRKENQ-----G 208
                                                                                                                                                                             220 EMSGIMIMLAVILPILAFFILLATVFSCIW---KSHPSICRKIGSLIKRRPQGEGPNPVAG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lung cancer;
MEDLINE-98151033; PubMed=9492069;
MEDLINE-98151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaquchi K., Kuriyama M., Ranno T., Murakami A., Isuda E., Morinaga T., Higashio K.;
Identity of Costeoolastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor
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MEDLINE-98238645; PubMed=9571159;
Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
Morinaga T., Tsuda E., Higashio K.;
                                                                                                                                                                                                                                                                                                                                               Tilb_HUMAN STANDARD; PRT; 401 AA.
000300; 060236; 09UHP4;
15-JUN-2002 (Rel. 41, Last sequence update)
(Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor."; Eur. J. Biochem. 254:685-691(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
RCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFC-----NSTVCE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
MEDLINE-97262071; PubMed-9108485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
MEDLINE-98351569; PubMed-9688283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFRSFILB OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human)
                                                                                                                                                                                                                        209 SHESPILNP 217
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SEQUENCE (
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                                                                                                                                                172
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12;

Gaps

79;

Indels

82; DB 1;

Local Similarity

Best Loca Matches

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63;

Length 435;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBDNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow. Detected at very low levels in brain, placenta and skeletal muscle. Highly expressed in fetal kidney, liver and lung.
-1- INDUCTION: Upregulated by increasing calcium-concentration in the medium and estrogens. Downregulated by glucocorticoids.
-1- PTM: N-glycosylated. Contains slalic acid residues.
-1- PTM: N-terminus may be blocked.
-1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99269100; PubMed-9603945; Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C., Dul E., Appelbaum E.R., Eichman C., DiPrinalo R., Dodds R.A., James I.E., Rosenberg M., Lee J.C., Young P.R.; "Osteoprofegerin is a receptor for the cytotoxic ligand TRAIL."; J. Biol. Chem. 273:14363-14367(1998).
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MEDLINE=98148058; PubMed=9478964;
Yamaquchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
Morinaga T., Higashio K.;
"Characterization of structural domains of human osteoclastogenesis inhibitory factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hofbauer L.C., Neubauer A., Heufelder A.E.;
"Receptor activator of nuclear factor-kappaB ligand and osteoprotegerin: potential implications for the pathogenesis and treatment of malignant bone diseases.";
Cancer 92:460-470(2001).
                                                                                                                                   He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and expression of osteoprotegerin from Homo sapiens.";
Acta Biochim. Biophys. Sin. 31:680-684(1999).
                                                                                                                                                                                                                                                MEDLINE-97312536; PubMed-9168977;
Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
Morinaga T., Higashio K.;
"Isolation of a novel cytokine from human fibroblasts that
specifically inhibits osteoclastogenesis.";
Blochem. Blophys. Res. Commun. 234:137-142(1997).
    ot
                                                                                                                                                                                                                           SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
"Characterization of monomeric and homodimeric forms
                     osteoclastogenesis inhibitory factor.";
Biochem. Biophys. Res. Commun. 245:382-387(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 273:5117-5123(1998).
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                                                                                        SEQUENCE OF 22-393 FROM N.A.
                                                                                                                  FISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                              TRAIL BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKECTLTSNTKCKE--EGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKH-----
                                                                                                                                                                                                                              PROSITE; PSC0017; DEATH DOMAIN; FALSE_NEG.
PROSITE; PSC0652; TNFR_NGFR_1; 2.
PROSITE; PSC0050; TNFR_NGFR_2; 2.
Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 183; DB 1; Length 40; Pred. No. 1.1e-06; 35; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVOLVED IN DIMERIZATION.
BY SIMILARITY.
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EDF448B67D86C71E CRC64;
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THER-CYS 1.
THER-CYS 2.
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THER-CYS 4.
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AB008E21; BAA32076.1; JO3
BC030155; AAH30155.1; -.
AF134187; AAF20168.1; -.
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ProDom; PD000771; TNFR_C6; 1.
SWART; SW00005; DEATH; 1.
SWART; SW00208; TNFR; 4.
                                                         HSSP; P25942; 1CDF.
Genew; HGNC:11909; TNFRSF11B.
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25.9%;
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InterPro; IFR001368; TNFR_c6
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263
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401 AA;
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EMBL;
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Matches
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HSSP;
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AB002146; BAA25910.1; -. AB008822; BAA32076.1; -.

EMBL; EMBL;

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                                                                                                                                                                                          Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimmanco G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Campbell P., Sander S., Van G., Tarpley J., Hill D., Pattison W., Suggs S., Boyle W.J.;

"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by 1,25-dihdroxyvitamin D3 and parathyroid hormone.
-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.
                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
                                                                                                                                                                                                                                                                                                                                                                                "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capparelli C., Scully
                                                                   precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., s
Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
                                       15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B prec (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
                                                                                                                                                                                                                                                                                                                         AND ARG-296.
STRAIN-129/Ola, and NIH Swiss; TISSUE-Fibroblast;
MEDLINE-98382527; PubMed-9714833;
      401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21060987; PubMed-10952716;
                                                                                                                                                                   STRAIN-BALB/c, TISSUE-Kidney;
MEDLINE-97262071; Pubmed-9108485;
                      15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last seq
15-UUN-2002 (Rel. 41, Last sen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                            of bone density.";
Cell 89:309-319(1997).
                                                                                               Mus musculus (Mouse).
                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and in embryo.
                                                                                                                                 NCBI_TaxID=10090;
             008712; 070202;
   T11B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                    IN DIMERIZATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 TIQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVR-RKTLCVPCPD-HSYTDSWHT
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SIGNAL 1 21 BY SIMILARITY.
CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .) (POTENTIAL)
-> P (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 401;
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34; Mismatches 114; Indels
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
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Pred. No. 1.3e-06;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
        or send an email to license@isb-sib.ch)
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SMART; SM00208; TNFR; 4.
PROSITE; PS50017; DEATH-DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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InterPro; IPR001368; INFR_c6.
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ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45923 MW;
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